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Movahedi et al.

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(54) **TARGETING AND IN VIVO IMAGING OF TUMOR-ASSOCIATED MACROPHAGES**

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(22) Filed: **May 24, 2012**

(65) **Prior Publication Data**

US 2012/0301394 A1 Nov. 29, 2012

Related U.S. Application Data

(63) Continuation-in-part of application No. 13/065,794, filed on Mar. 29, 2011, now abandoned.

(60) Provisional application No. 61/341,356, filed on Mar. 29, 2010.

(51) **Int. Cl.**

A61K 51/10 (2006.01)

A61K 47/48 (2006.01)

C07K 16/28 (2006.01)

B82Y 5/00 (2011.01)

(52) **U.S. Cl.**

CPC **A61K 51/1027** (2013.01); **A61K 47/48484** (2013.01); **A61K 47/48561** (2013.01); **A61K 47/48761** (2013.01); **B82Y 5/00** (2013.01); **C07K 16/2851** (2013.01); **C07K 2317/22** (2013.01); **C07K 2317/35** (2013.01)

(58) **Field of Classification Search**

CPC **A61K 51/1027**; **A61K 47/48484**; **A61K 47/48561**; **A61K 47/48761**; **C07K 2317/22**; **C07K 16/2851**

See application file for complete search history.

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Primary Examiner — Ruixiang Li

(74) Attorney, Agent, or Firm — TraskBritt, P.C.

(57) **ABSTRACT**

The invention relates to activities and characteristics of tumor-associated macrophages (TAMs). In particular, immunoglobulin single variable domains are provided against markers of TAMs, and methods using the same for in vivo imaging of tumor cells, as well as cancer diagnostics and therapeutics.

14 Claims, 36 Drawing Sheets
(25 of 36 Drawing Sheet(s) Filed in Color)

FIG. 1

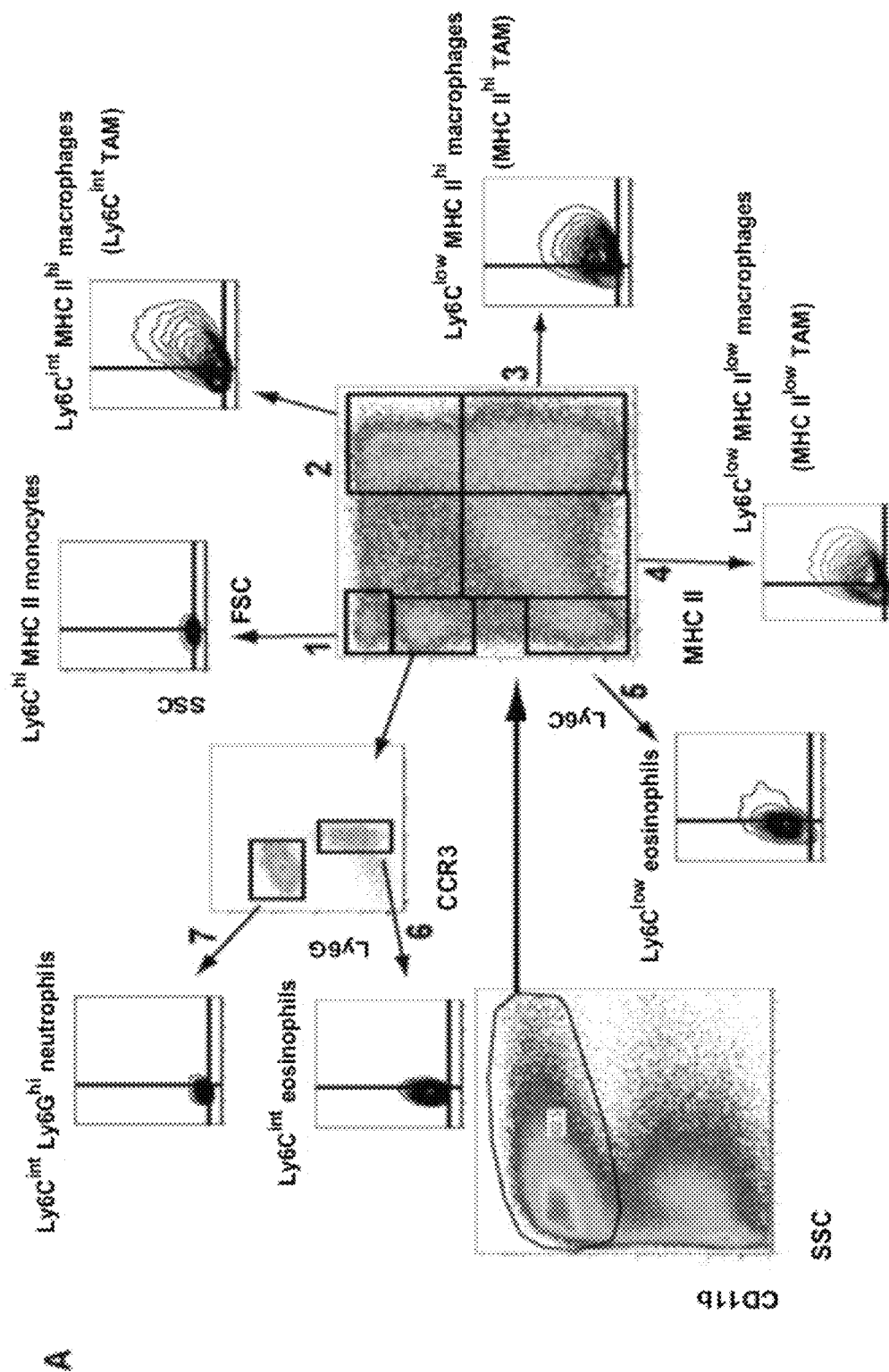


FIG. 1 (continued)

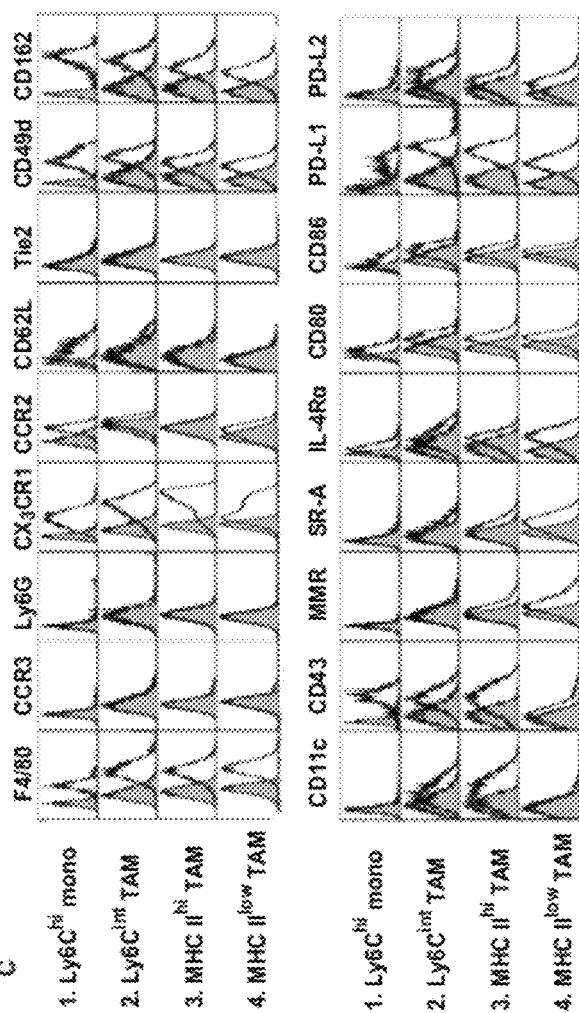
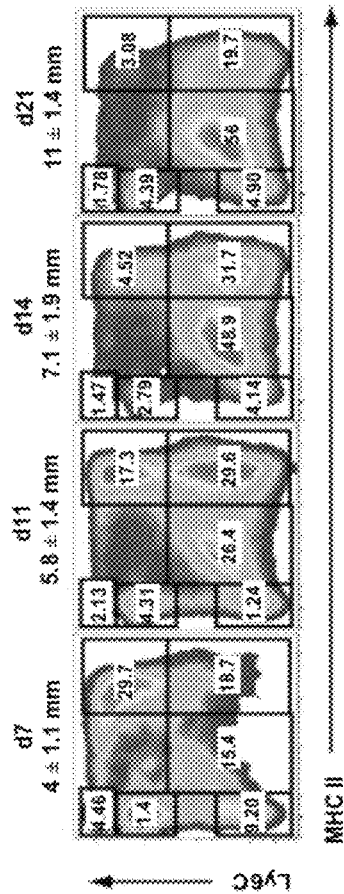


FIG. 2

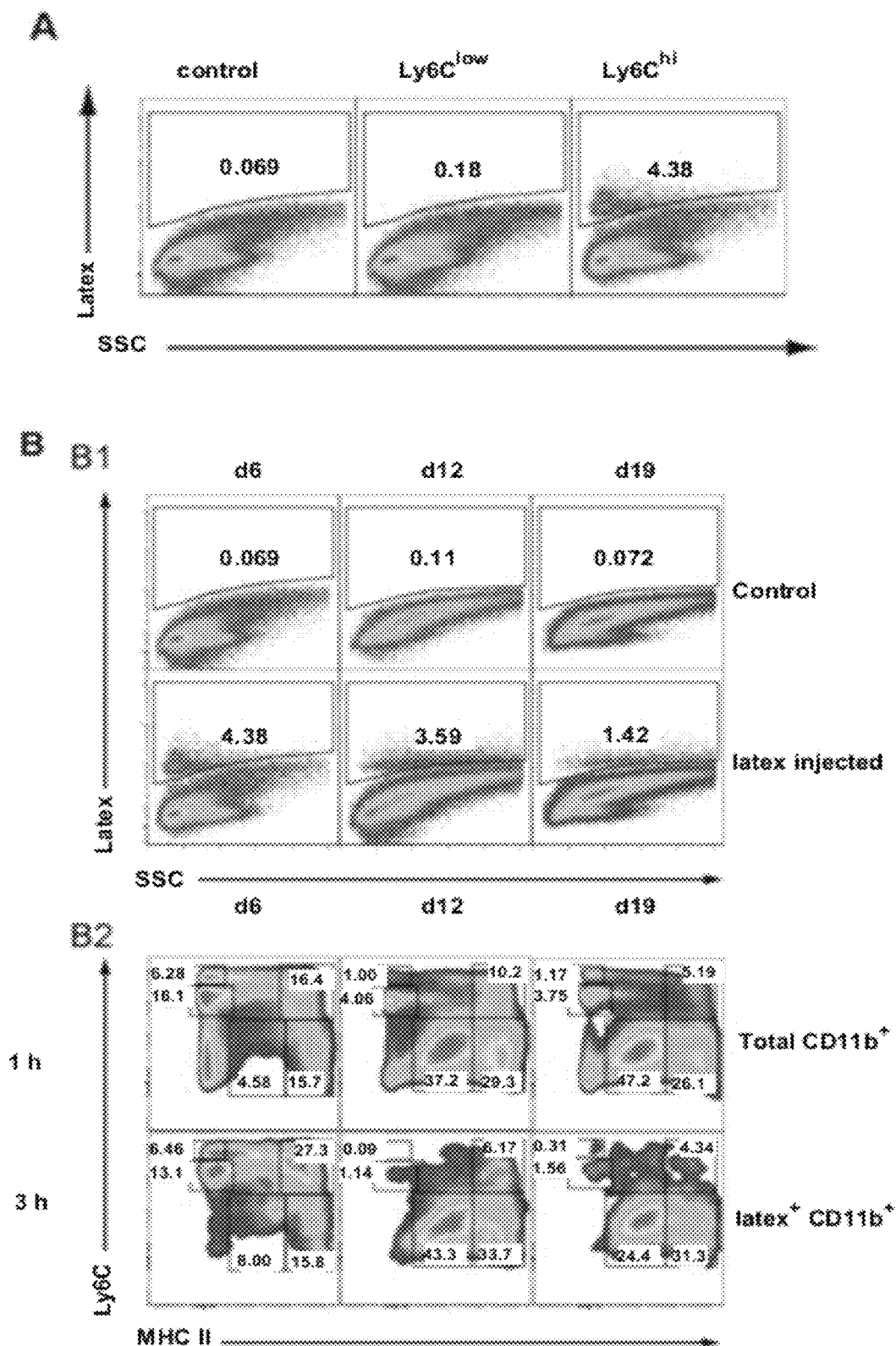


FIG. 2 (continued)

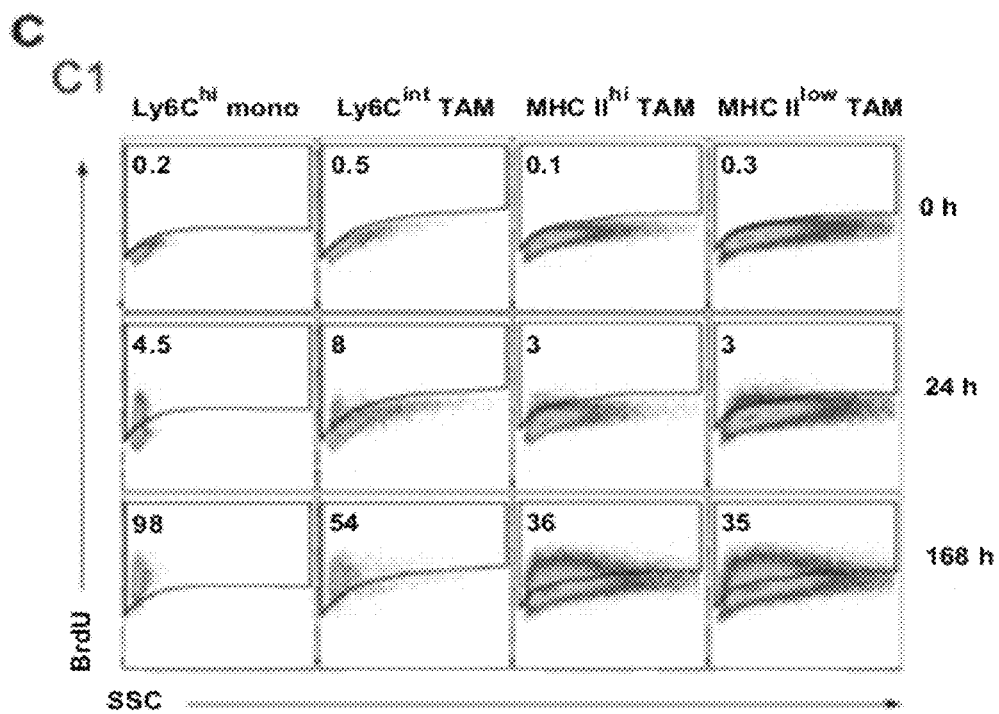


FIG. 2 (continued)

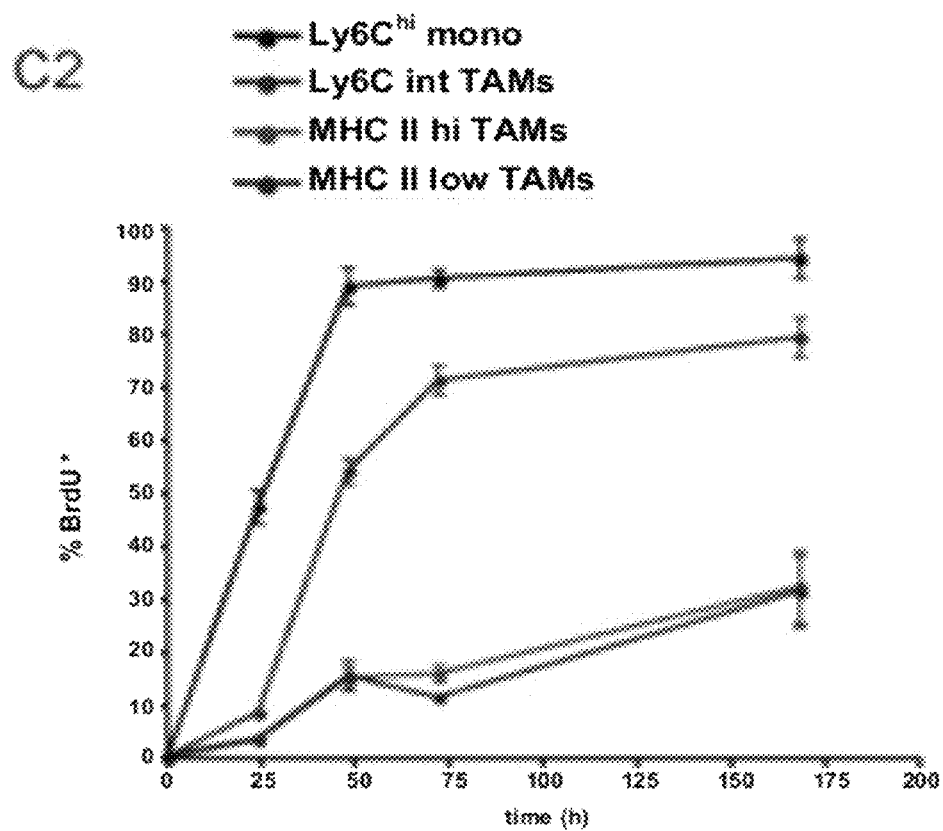
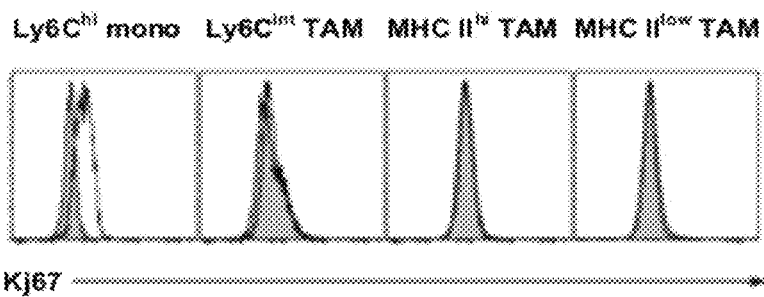
**D**

FIG. 3

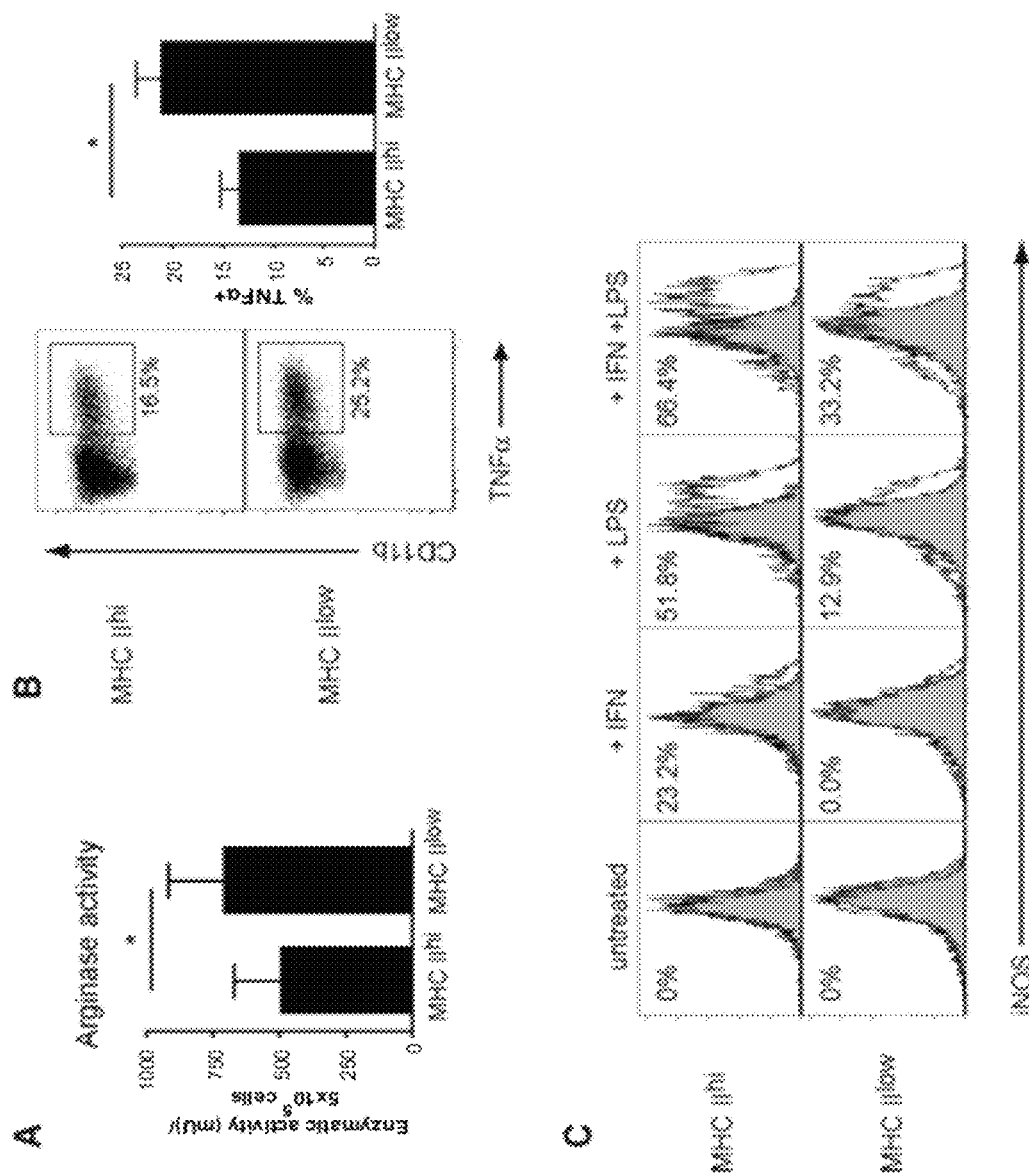


FIG. 4

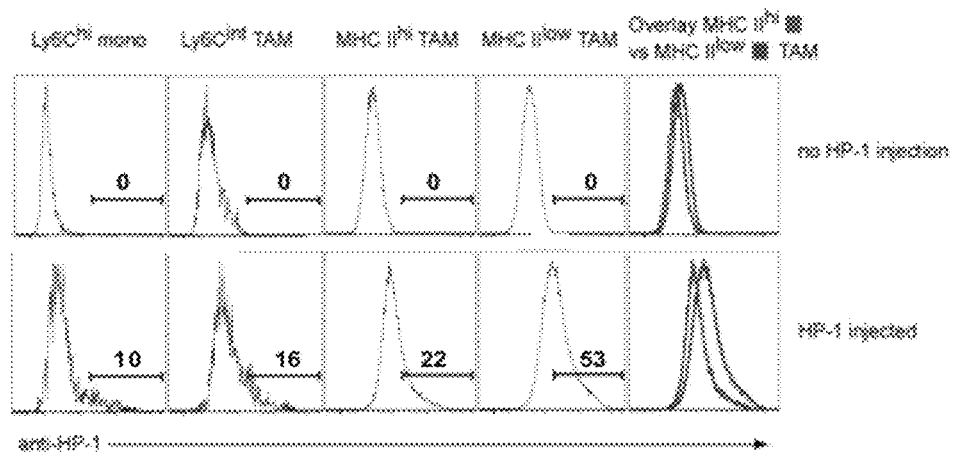
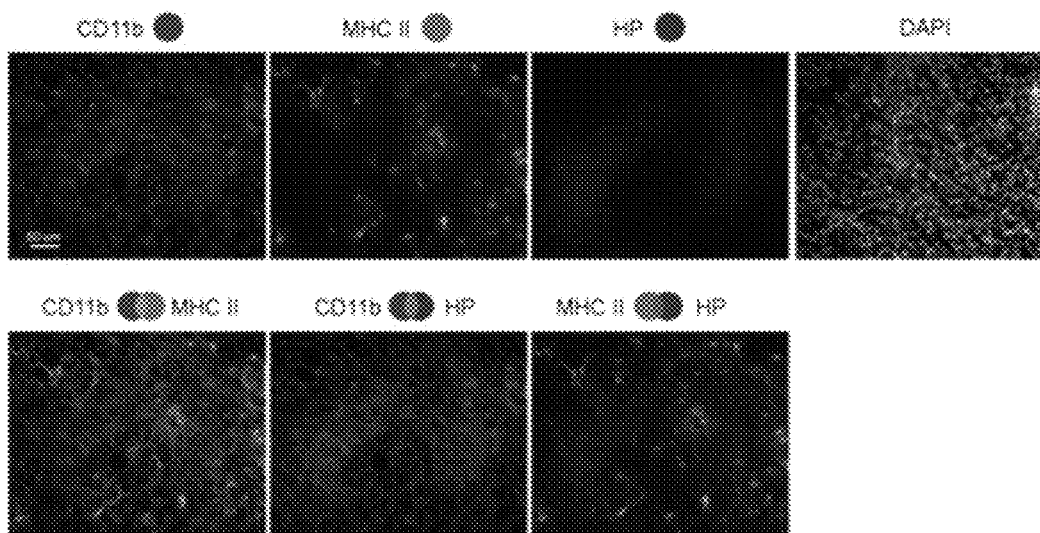
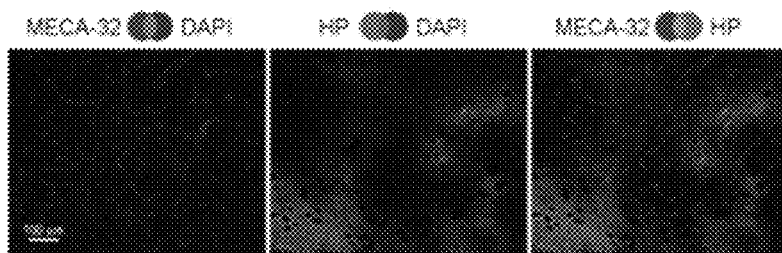


FIG. 5

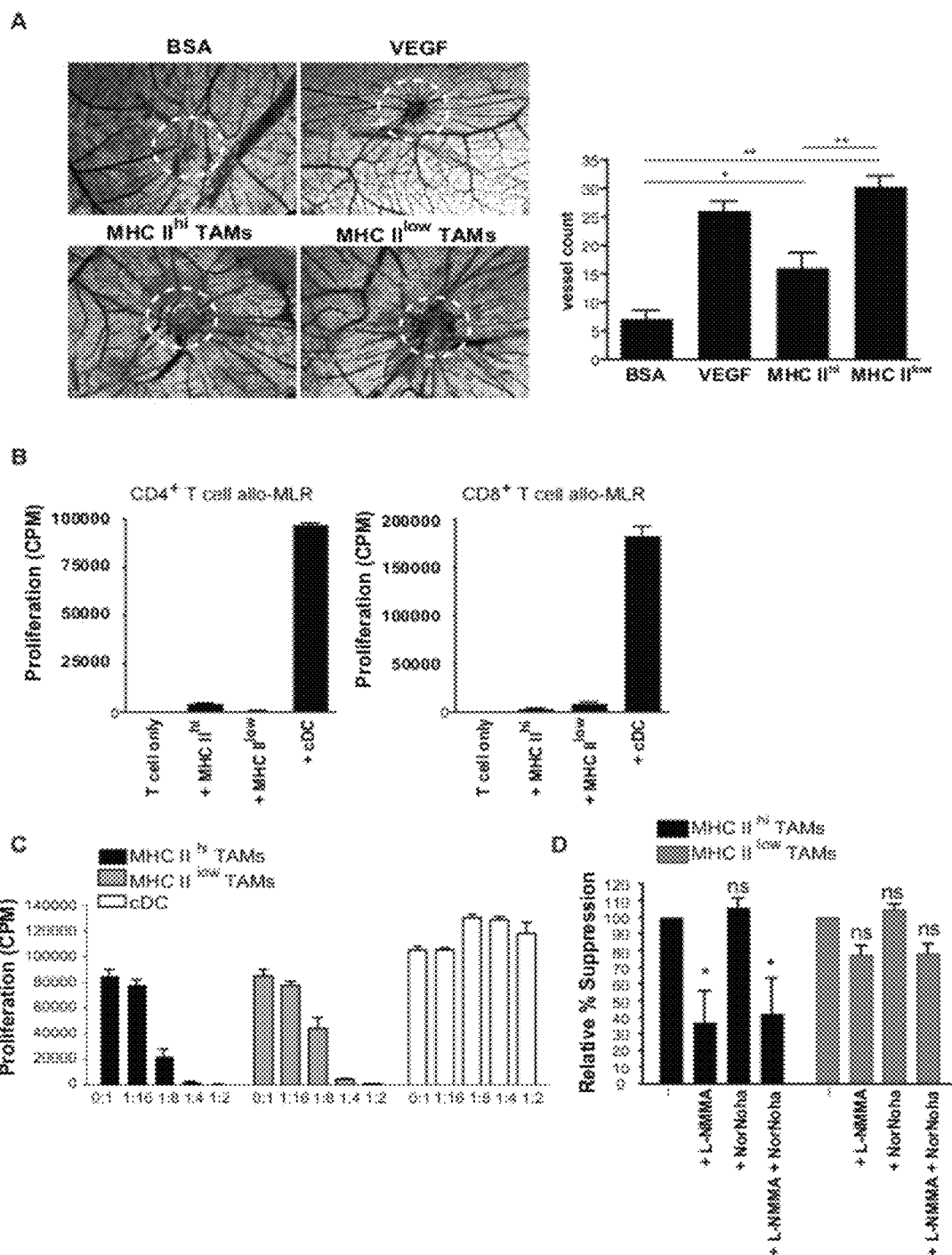


FIG. 6

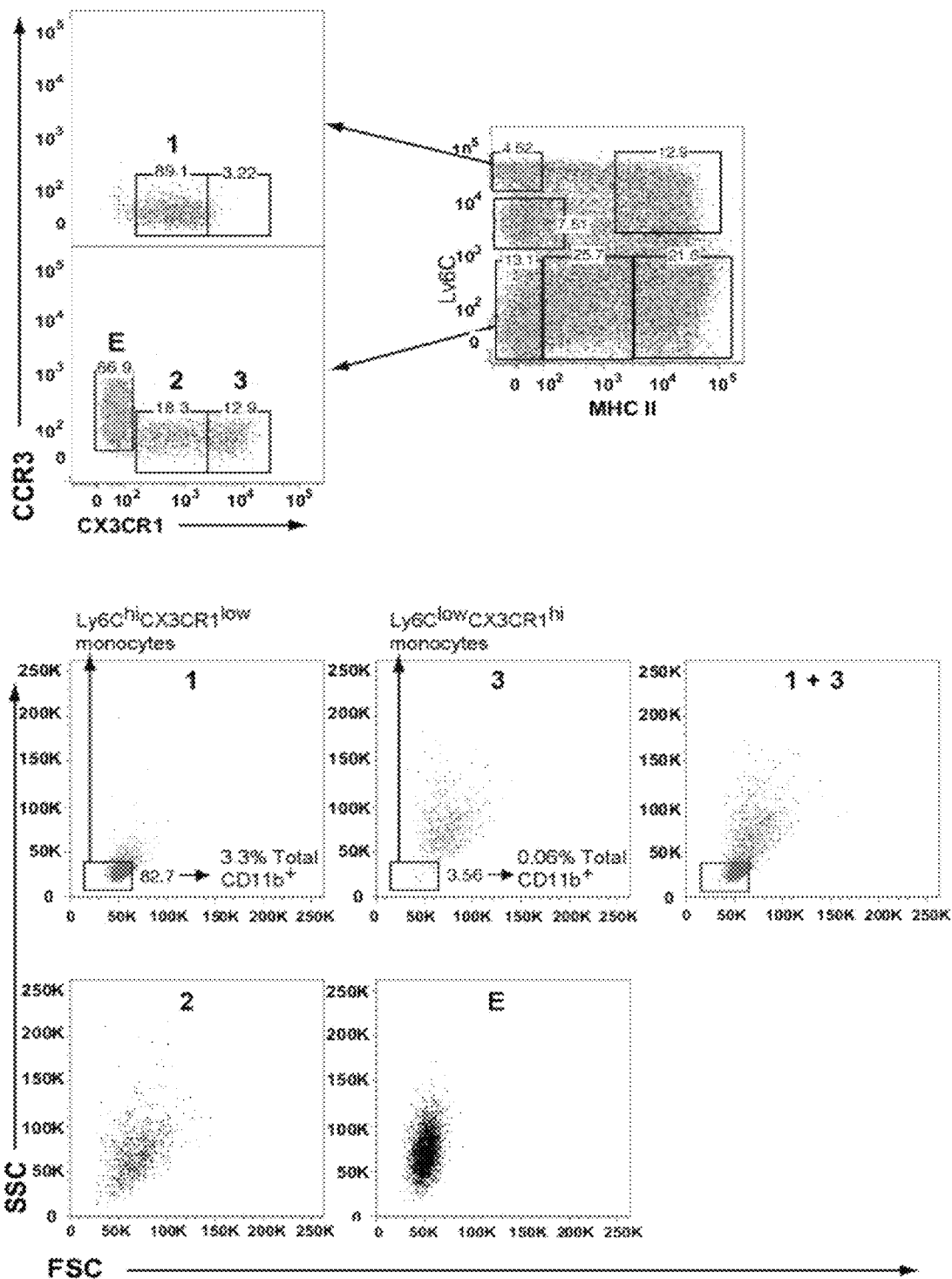


FIG. 7

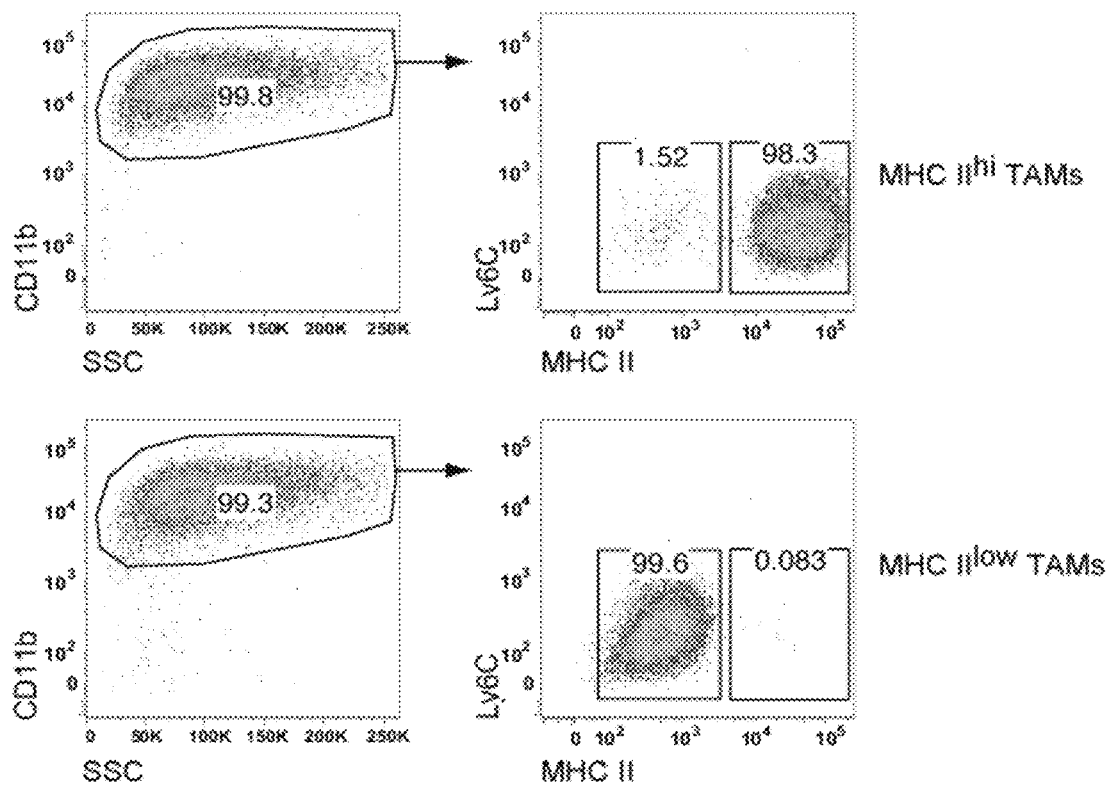
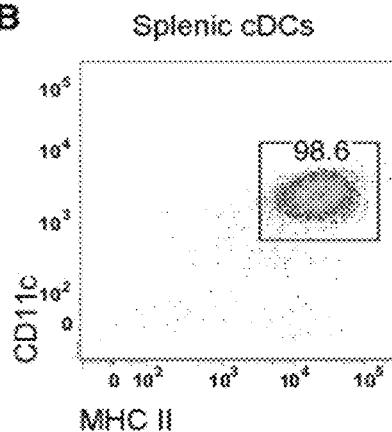
A**B**

FIG. 8

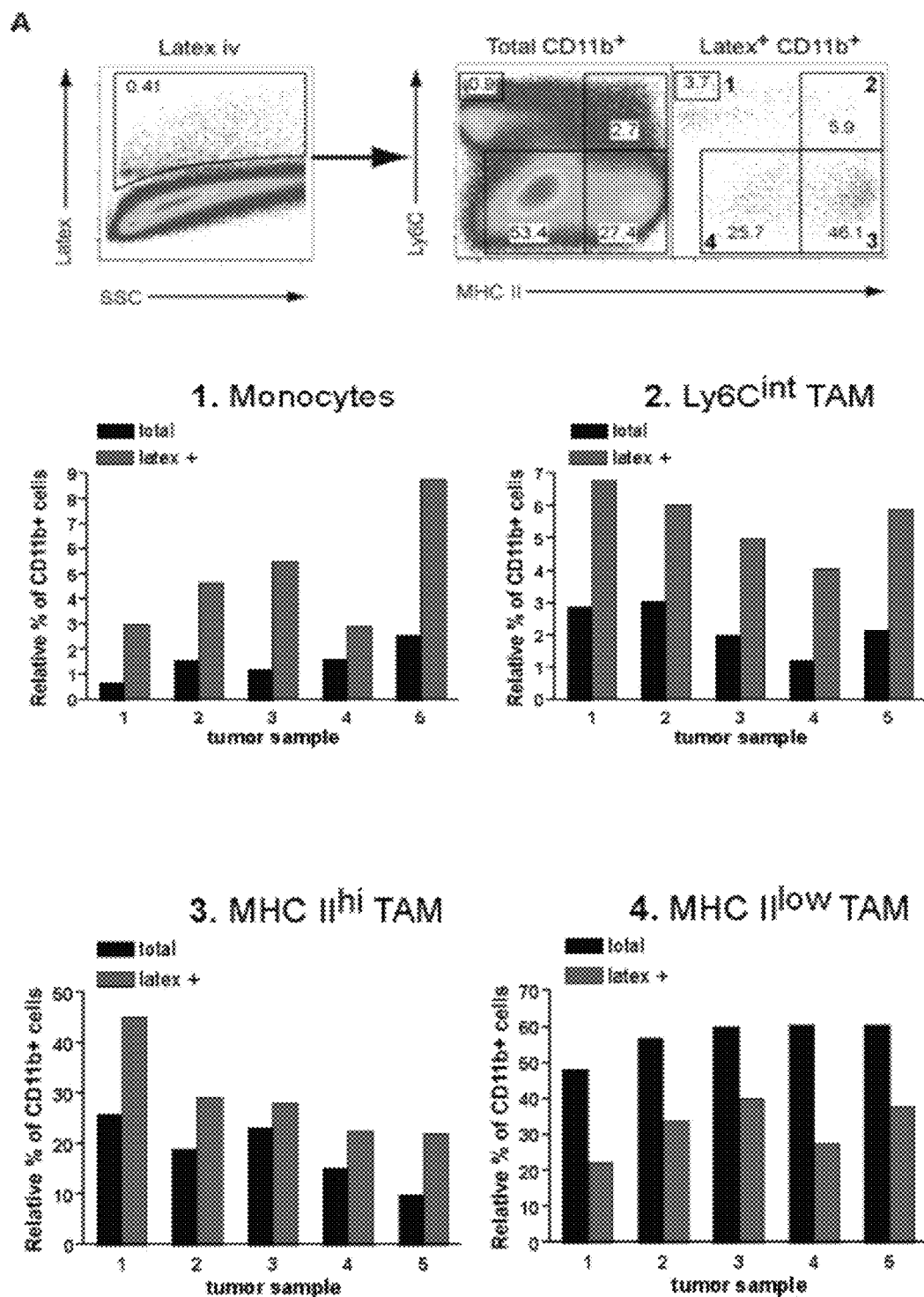


FIG. 8 (continued)

B

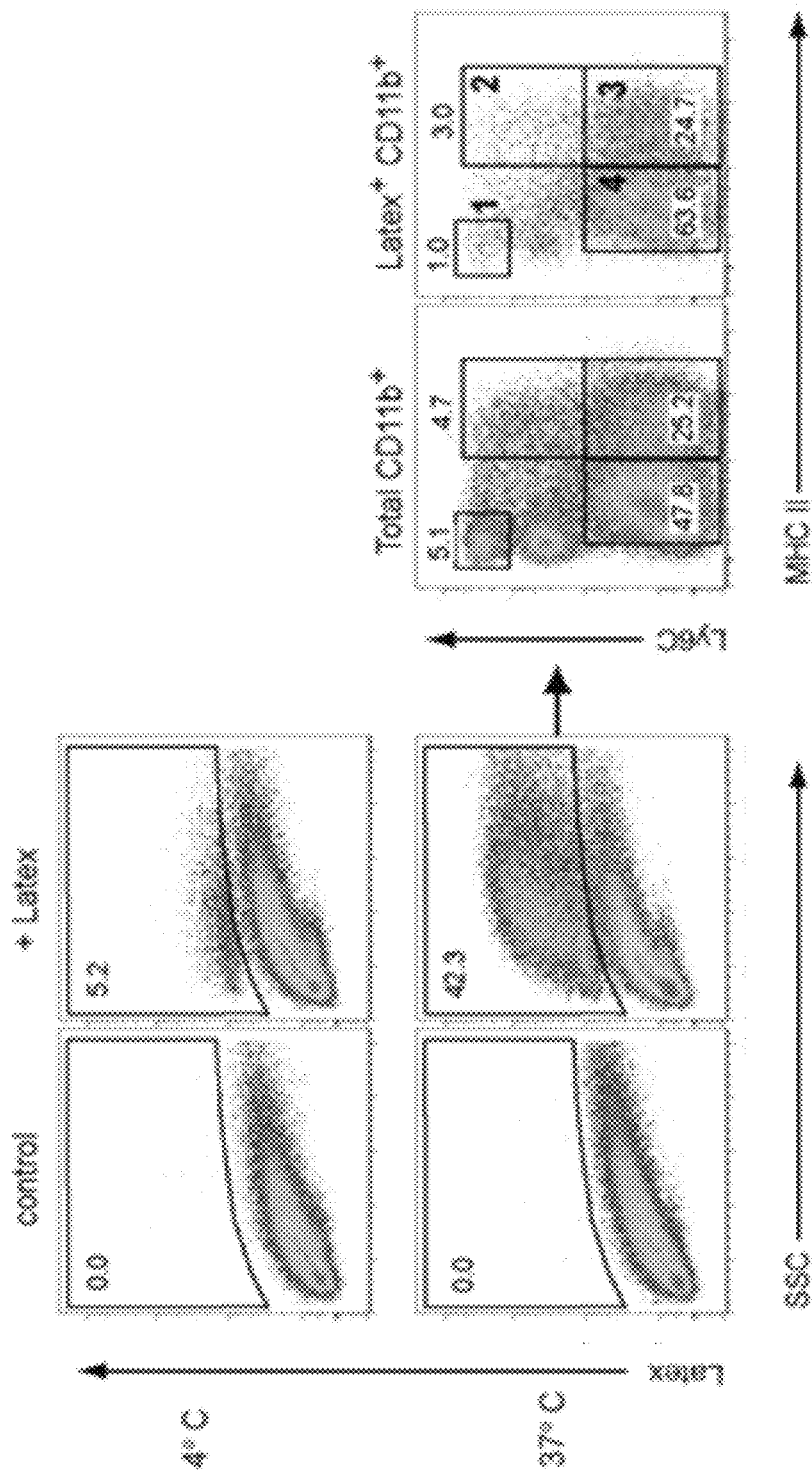


FIG. 8 (continued)

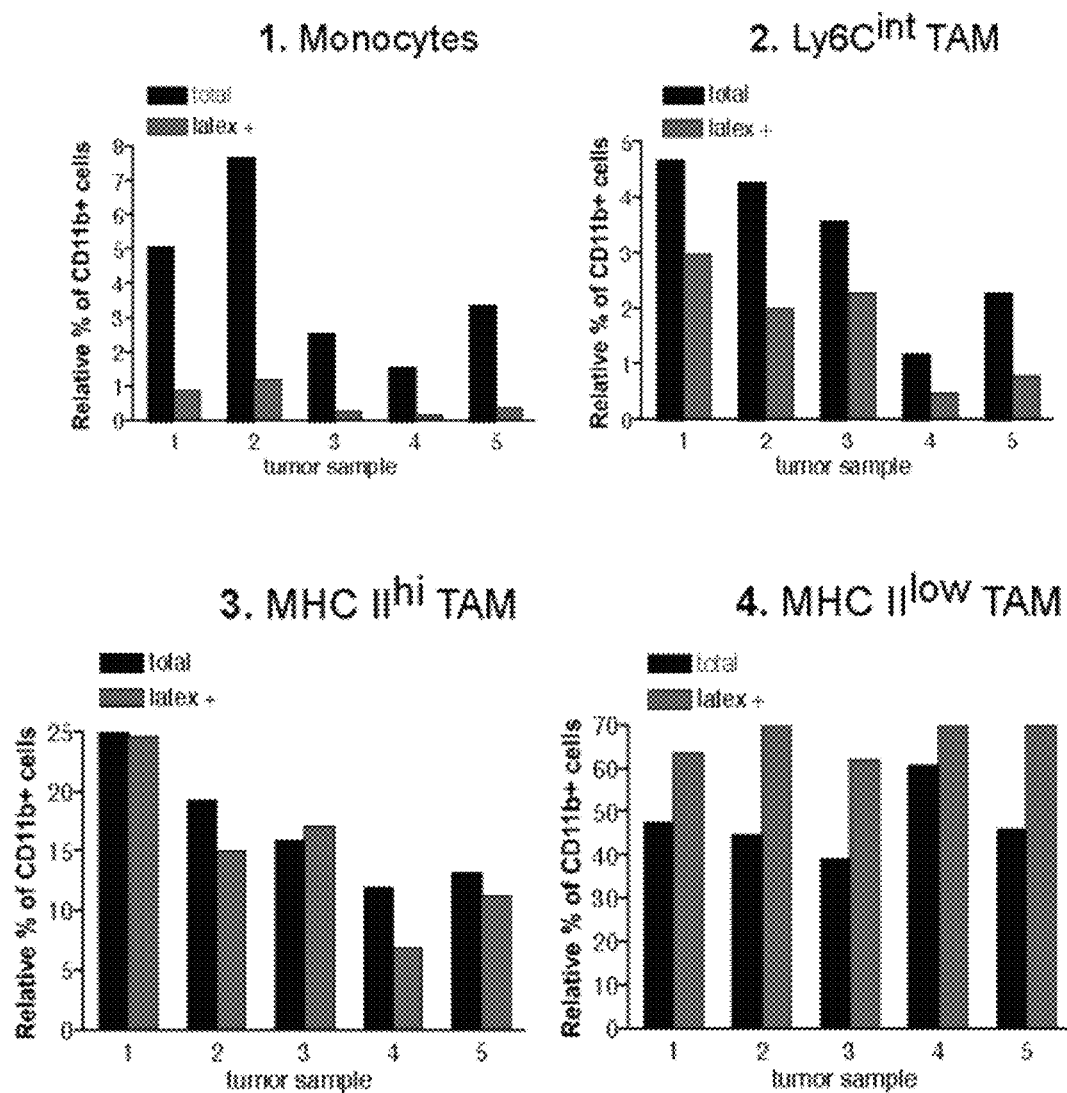


FIG. 9

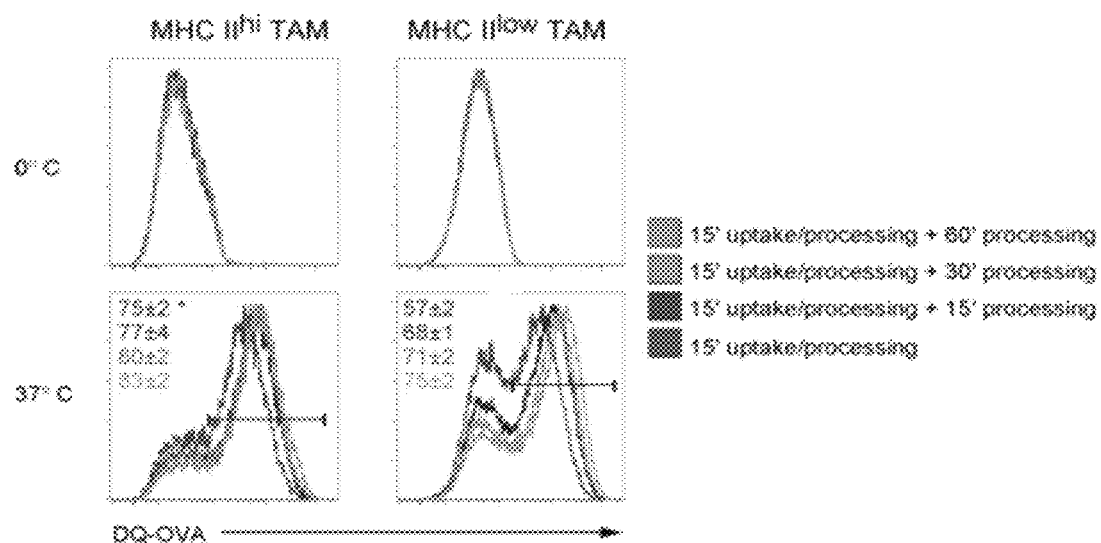


FIG. 10

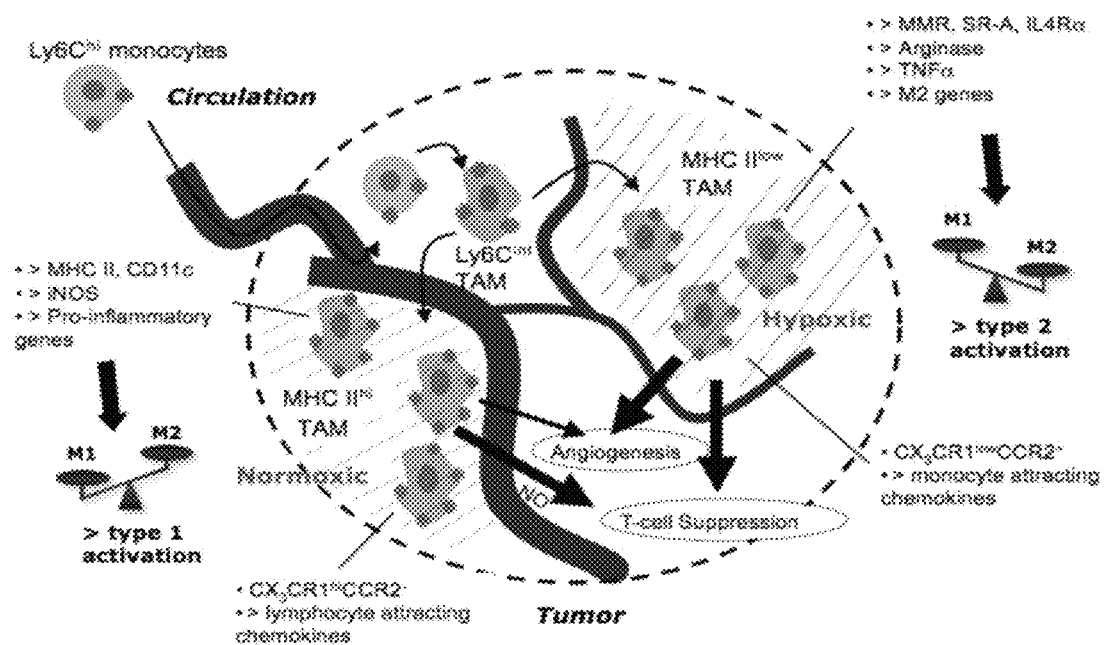


FIG. 11

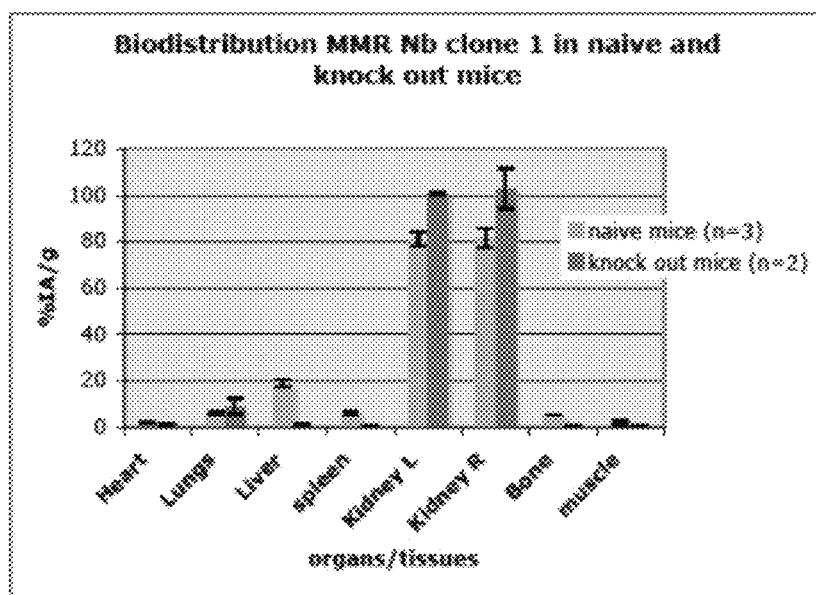


FIG. 12

%IA/g dissected tissue 1.5h i.v. injection ^{99m}Tc -Nbs

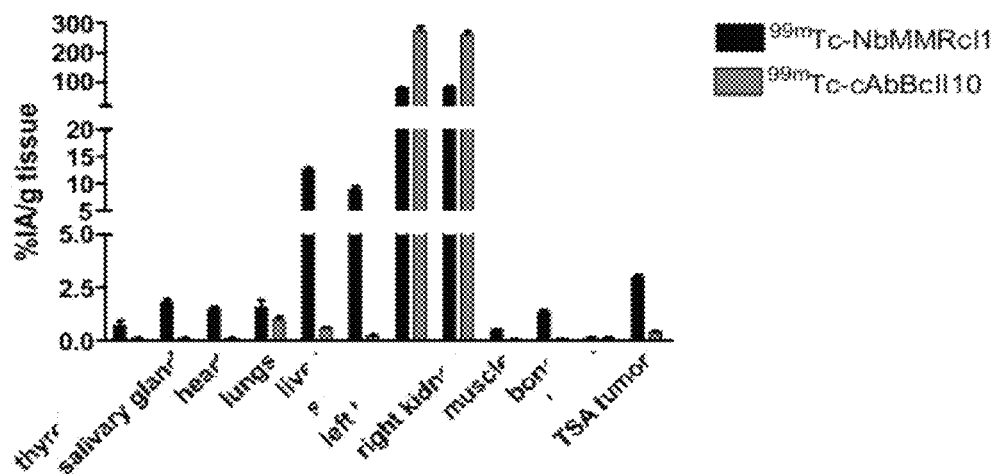


FIG. 13

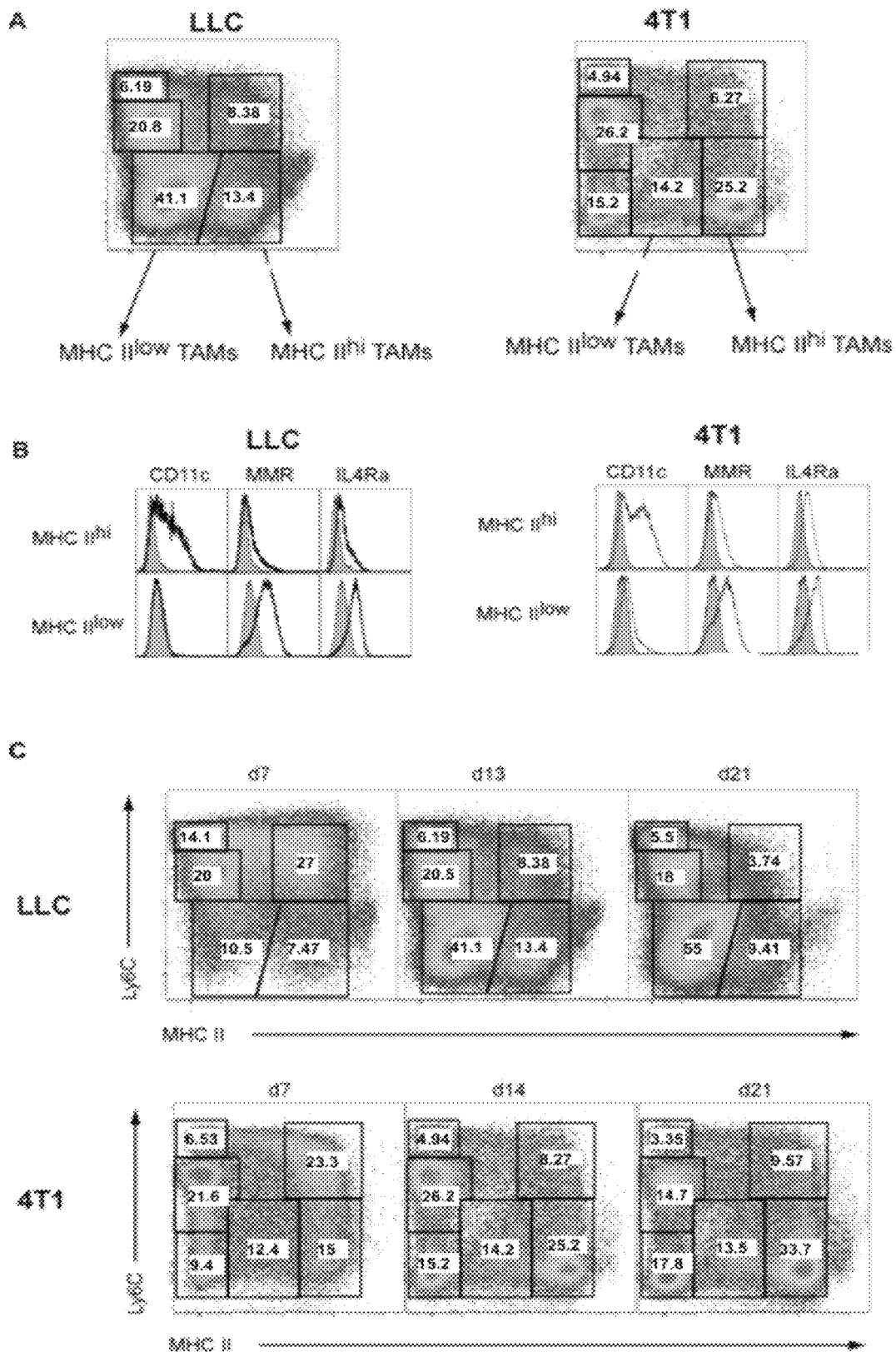


FIG. 14

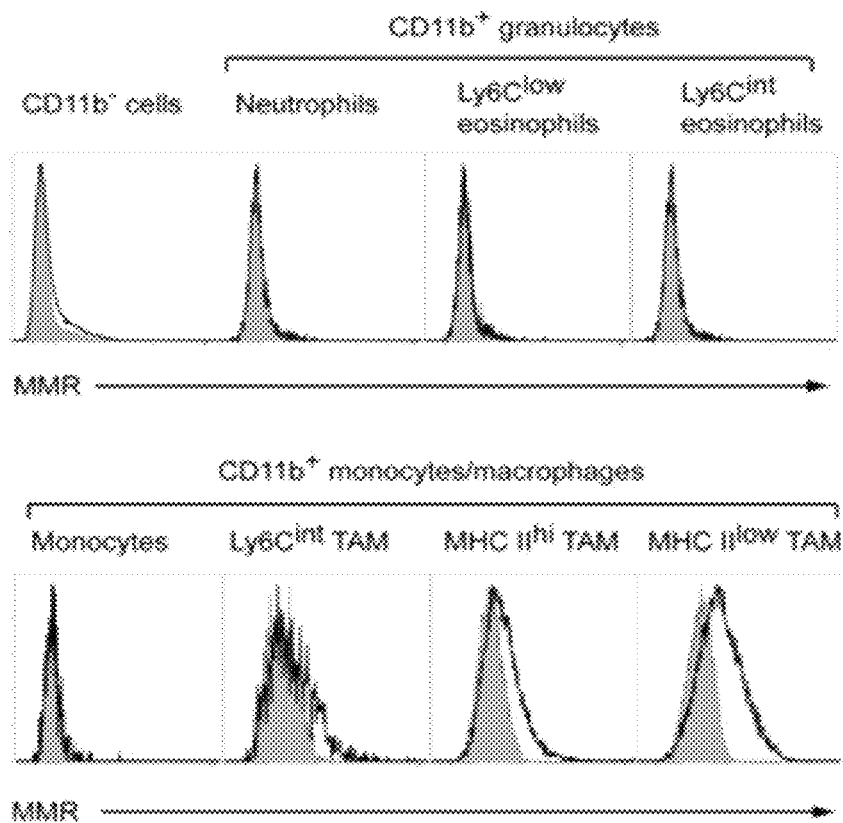


FIG. 15

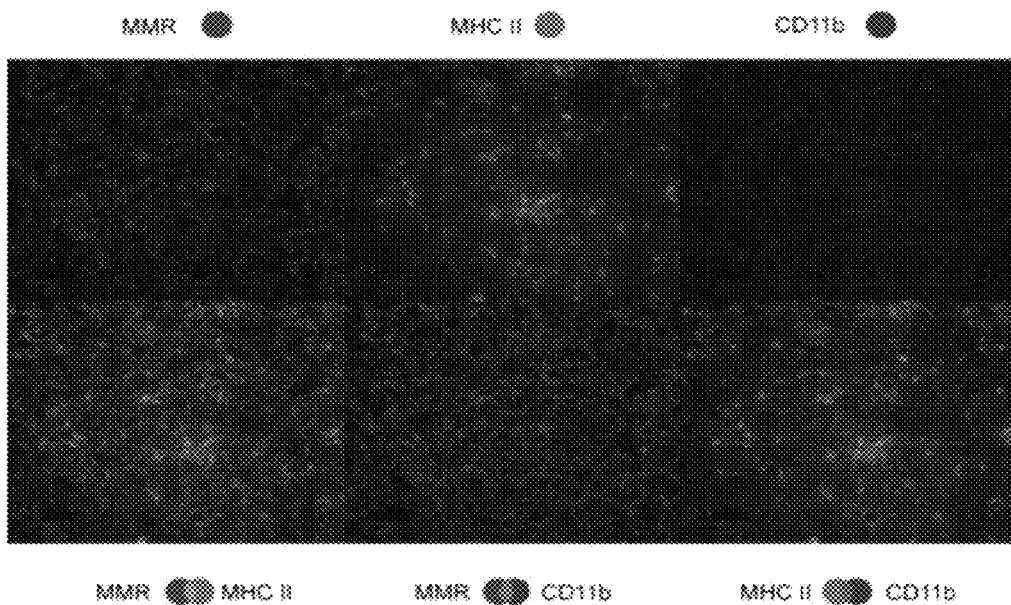


FIG. 16

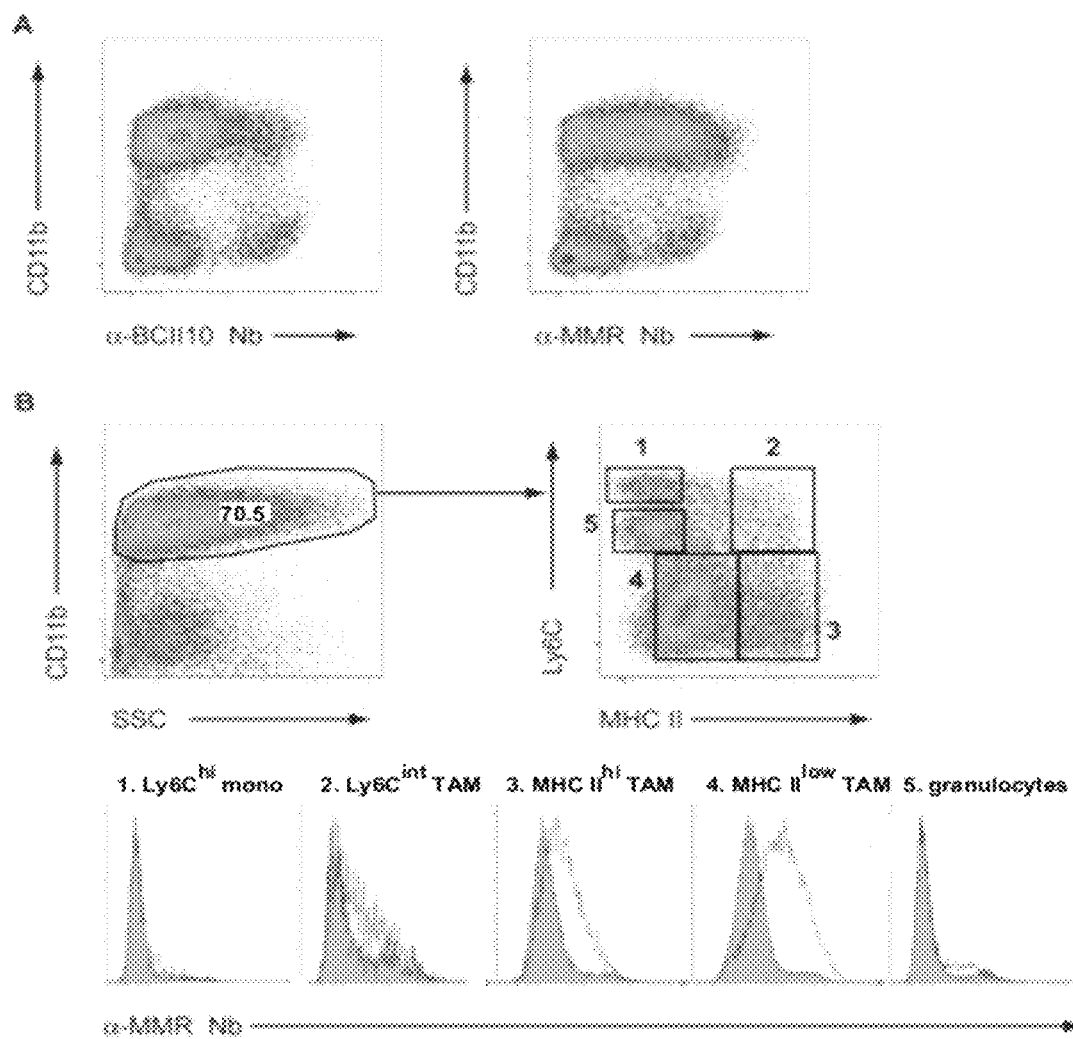


FIG. 17

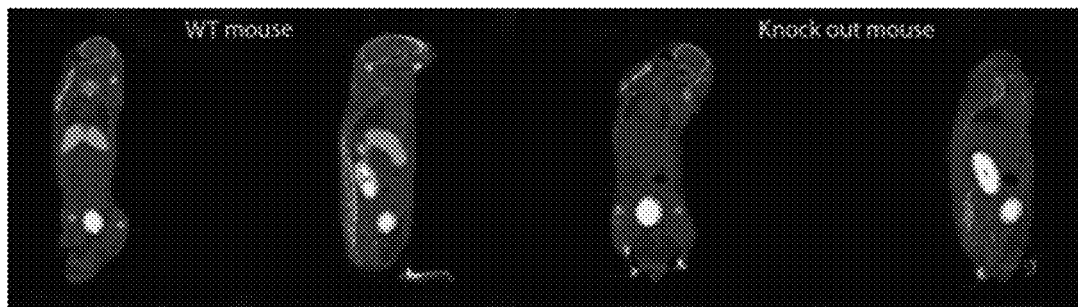


FIG. 18

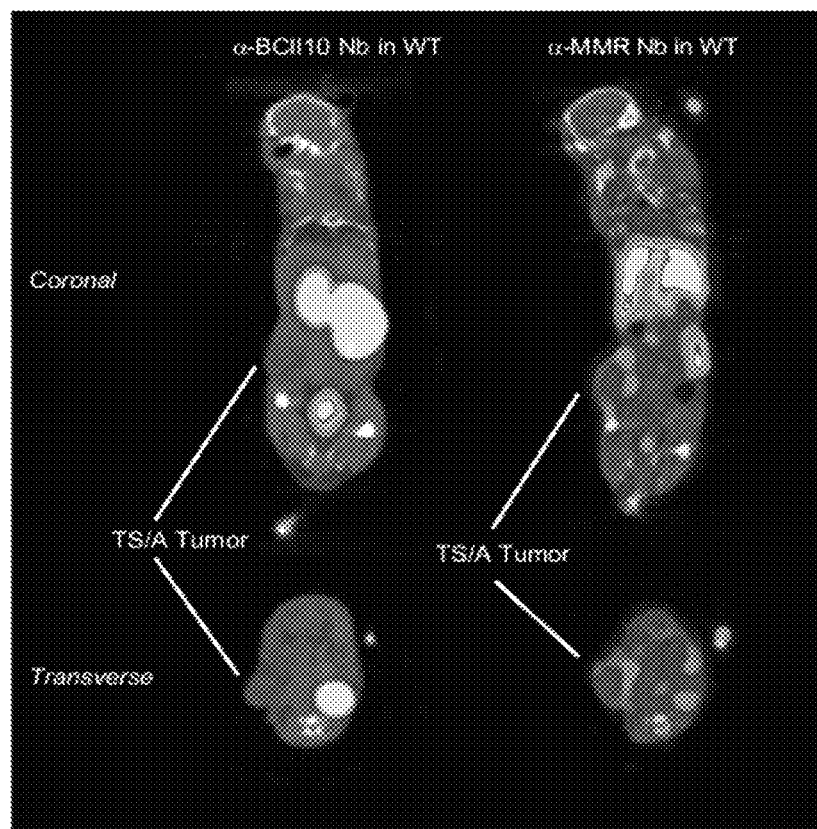


FIG. 19

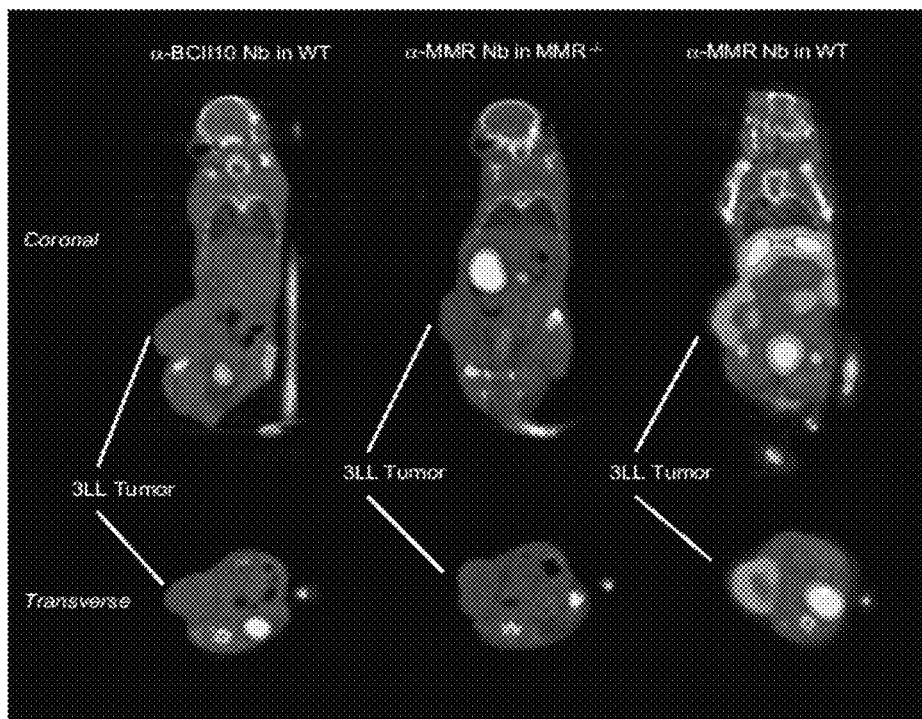


FIG. 20

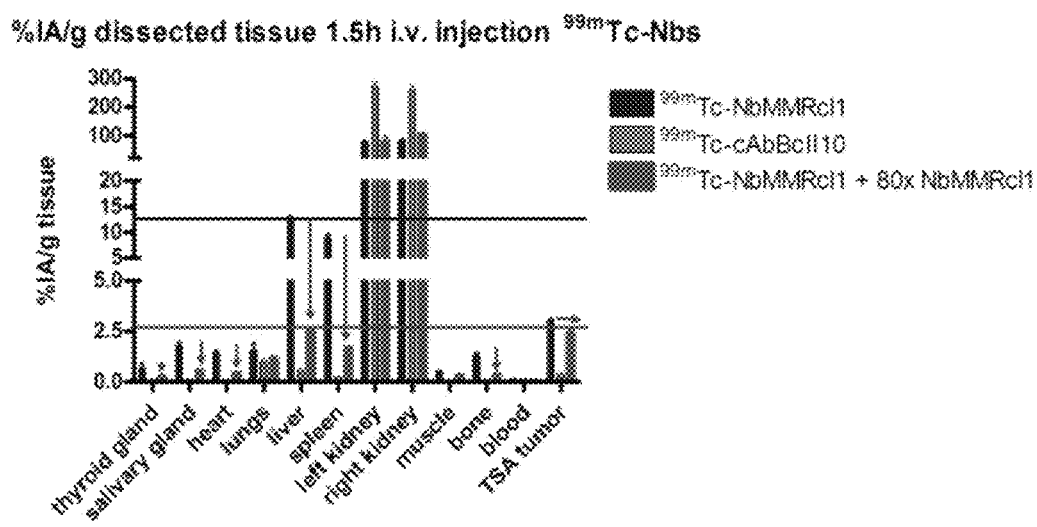


FIG. 21

%IA/g dissected tissue 3h i.v. injection ^{99m}Tc -Nbs

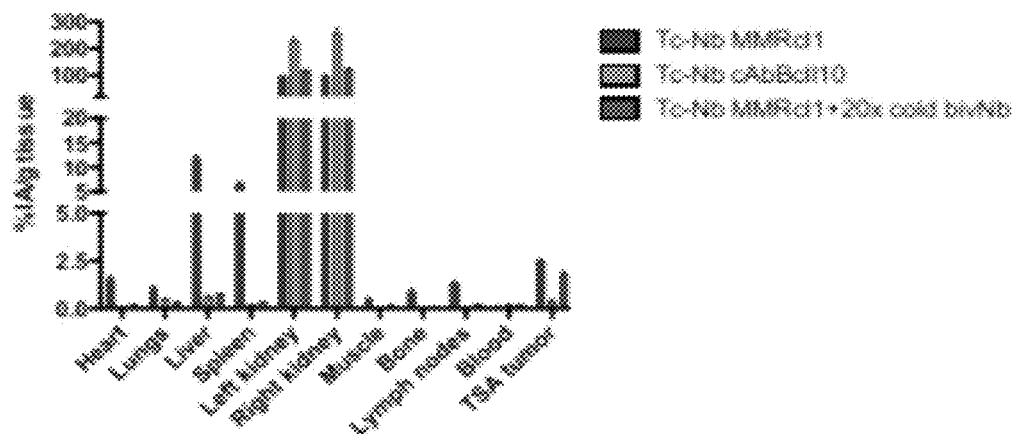


FIG. 22

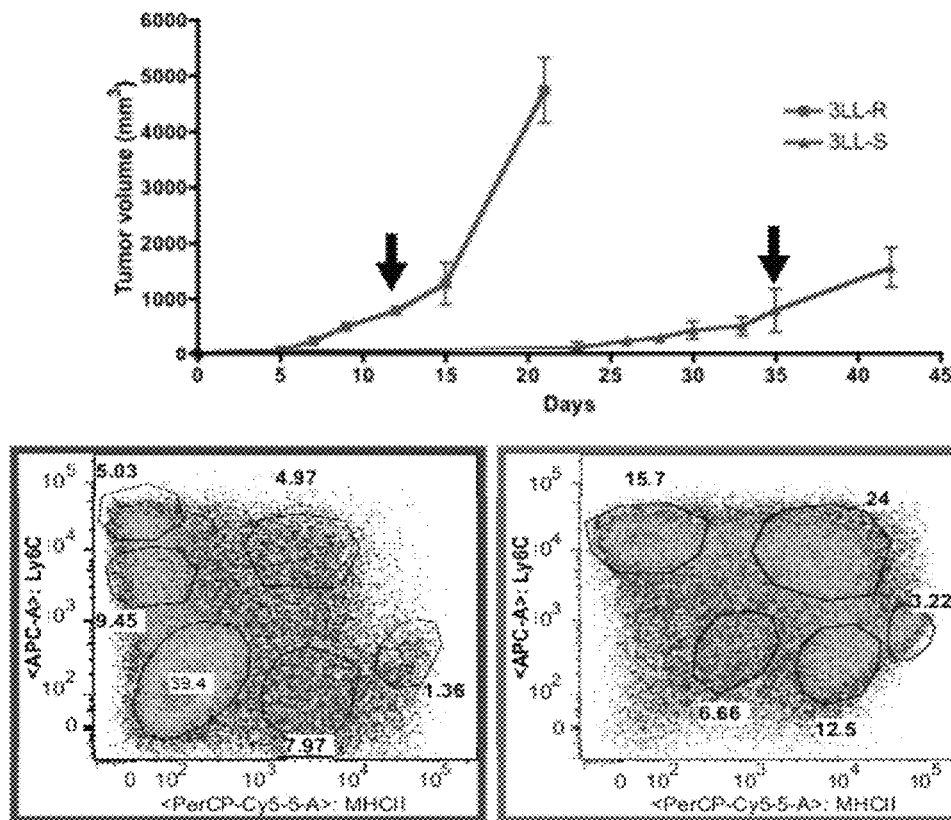


FIG. 23

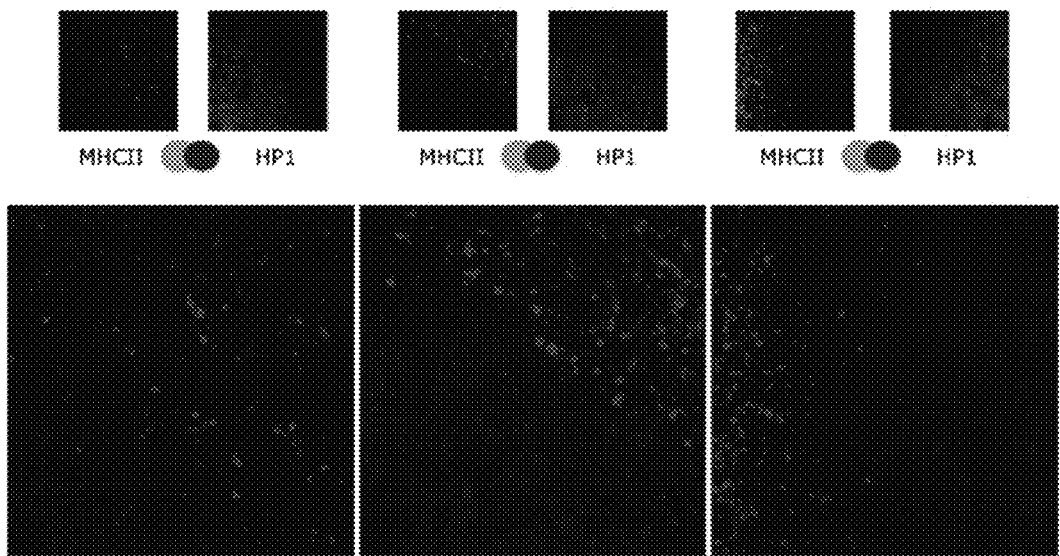


Figure 24

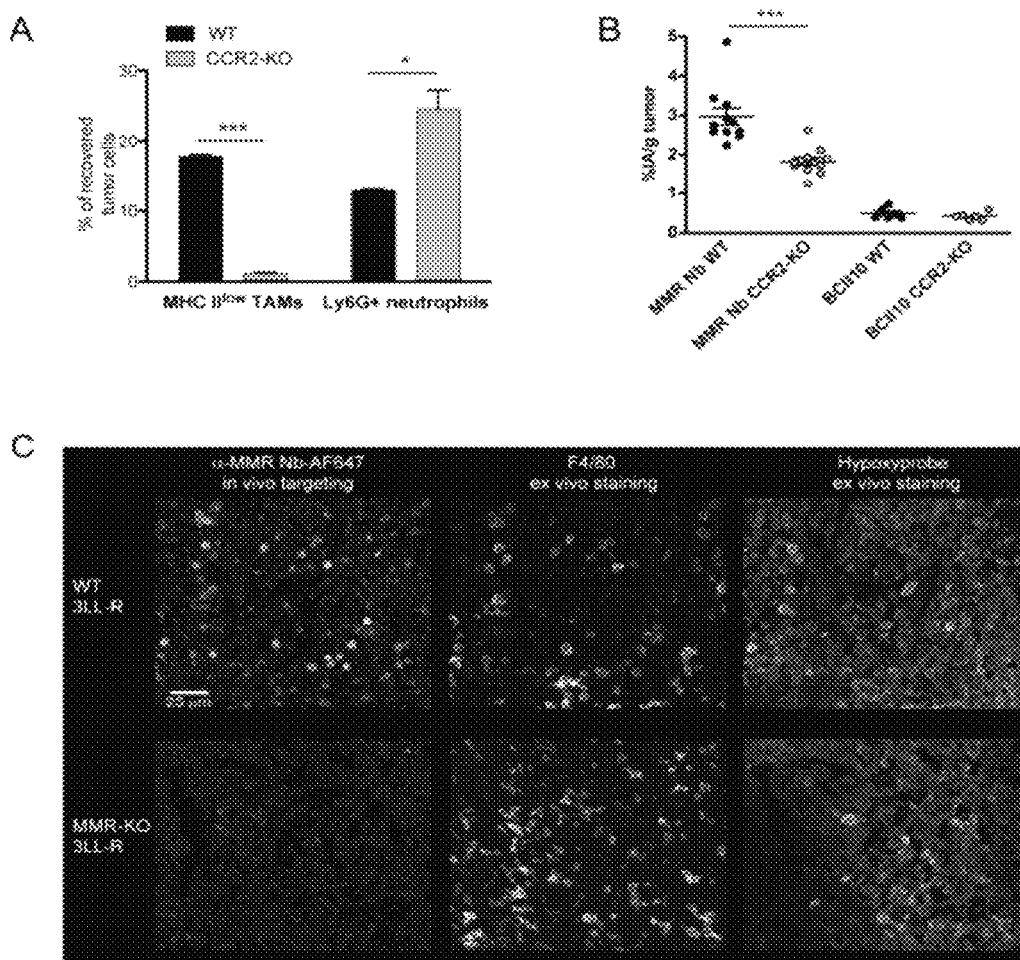


FIG. 24 (continued)

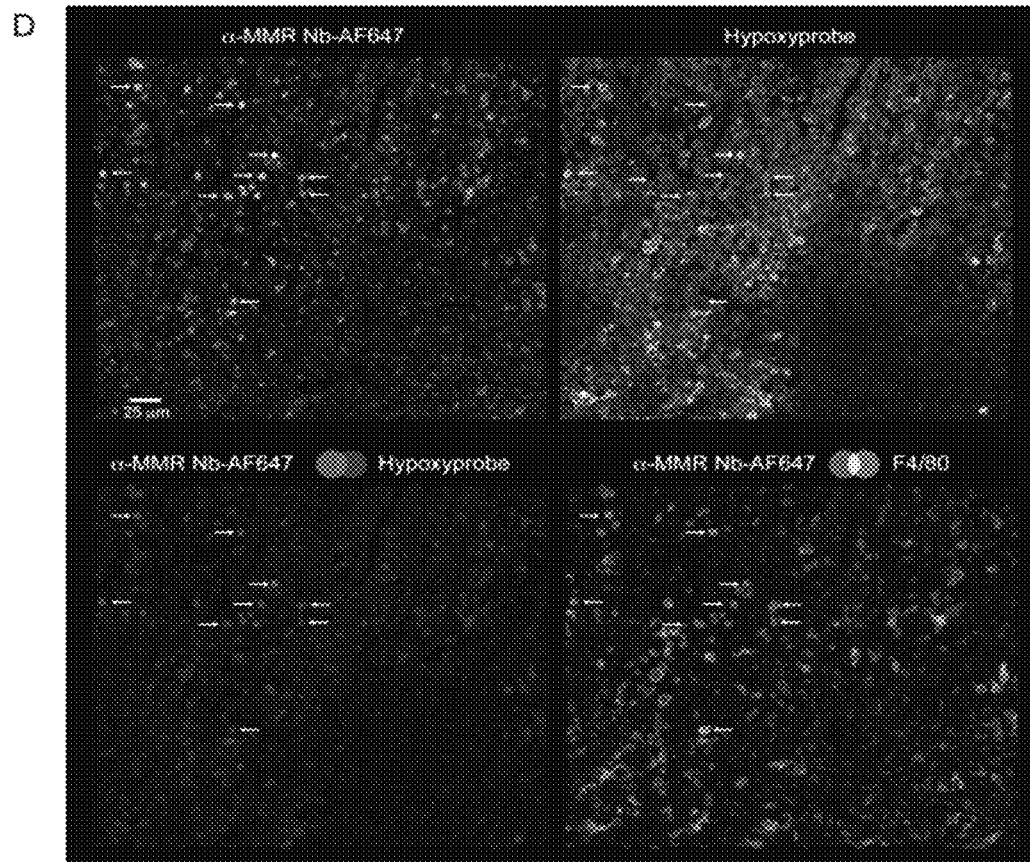
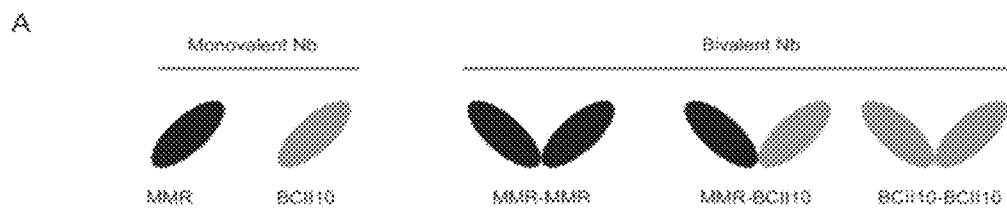


Figure 25



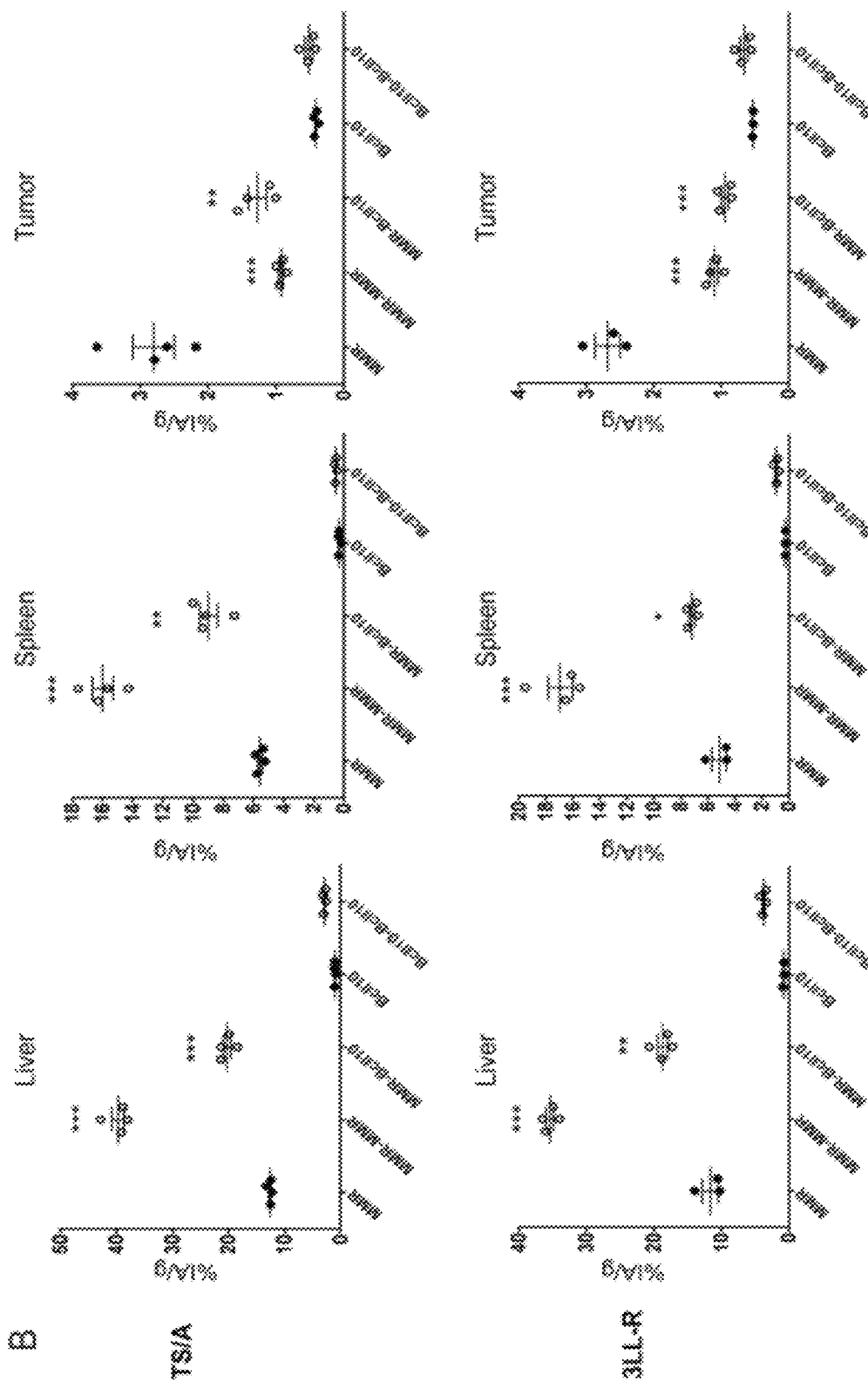


Fig. 25 (continued)

FIG. 25 (continued)

C

C1

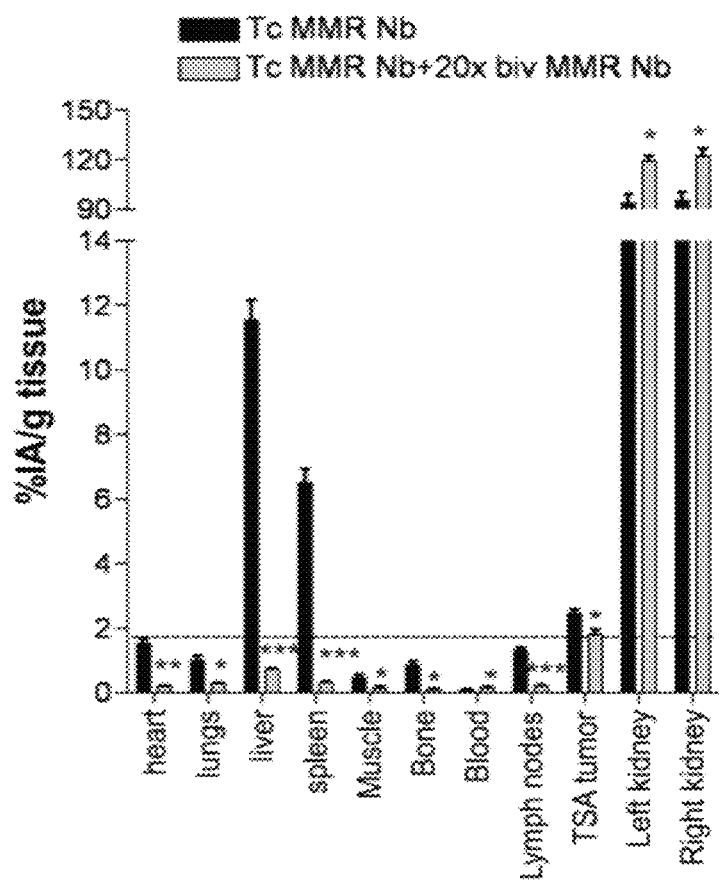
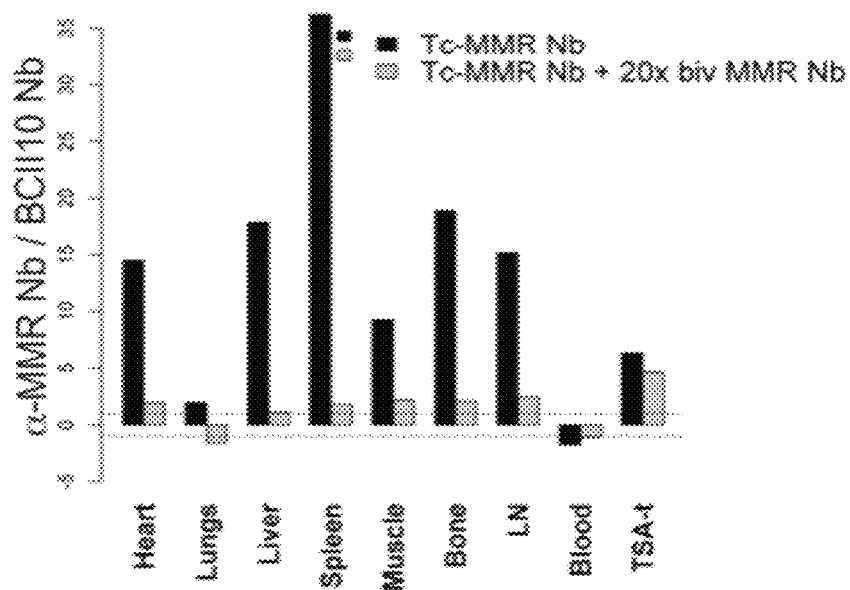


FIG. 25 (continued)

C2



C3

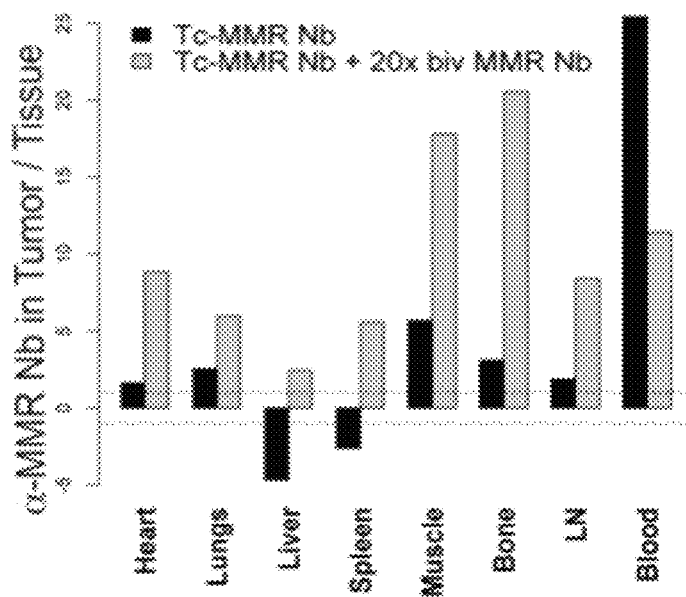


Figure 26

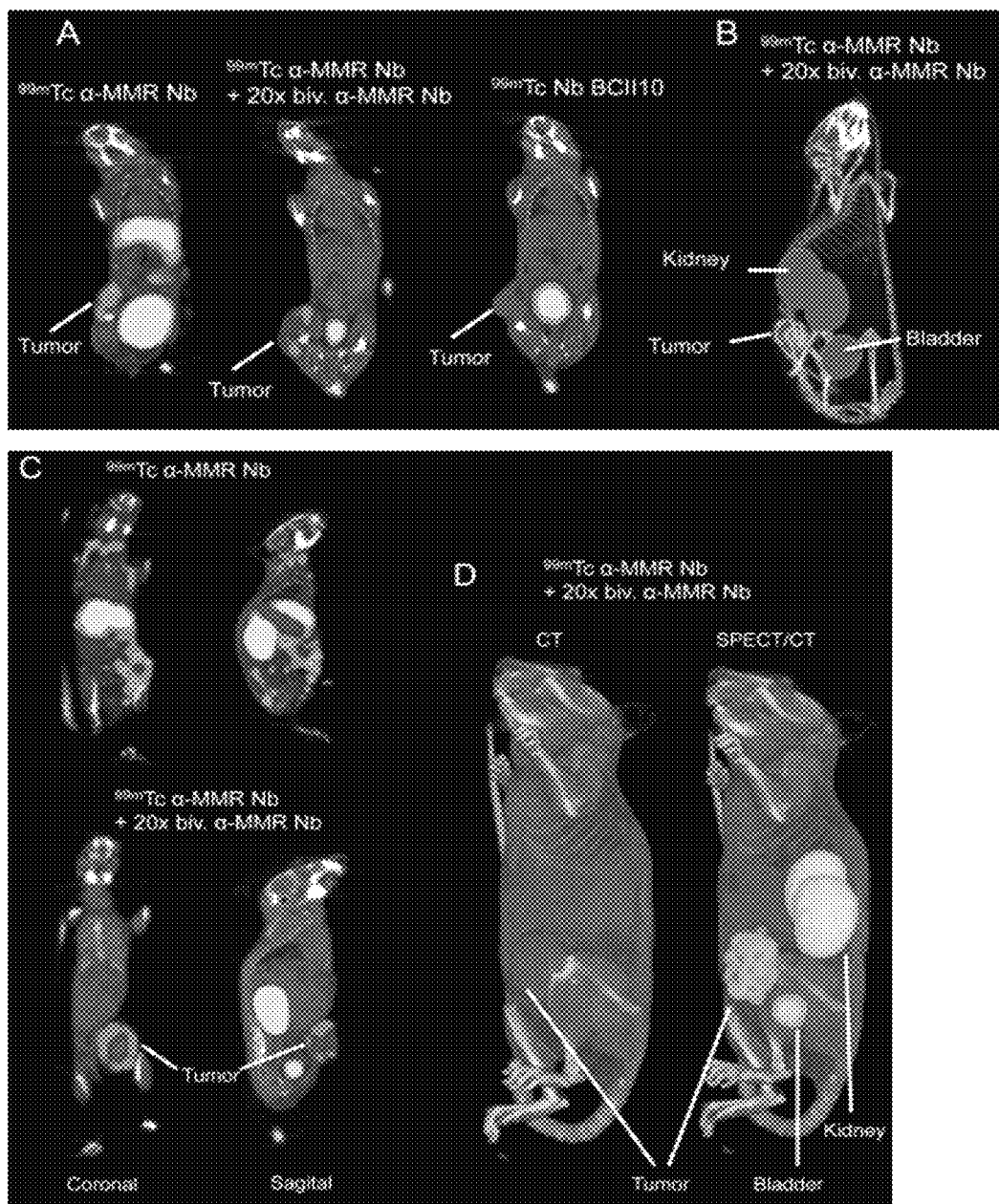


Figure 27

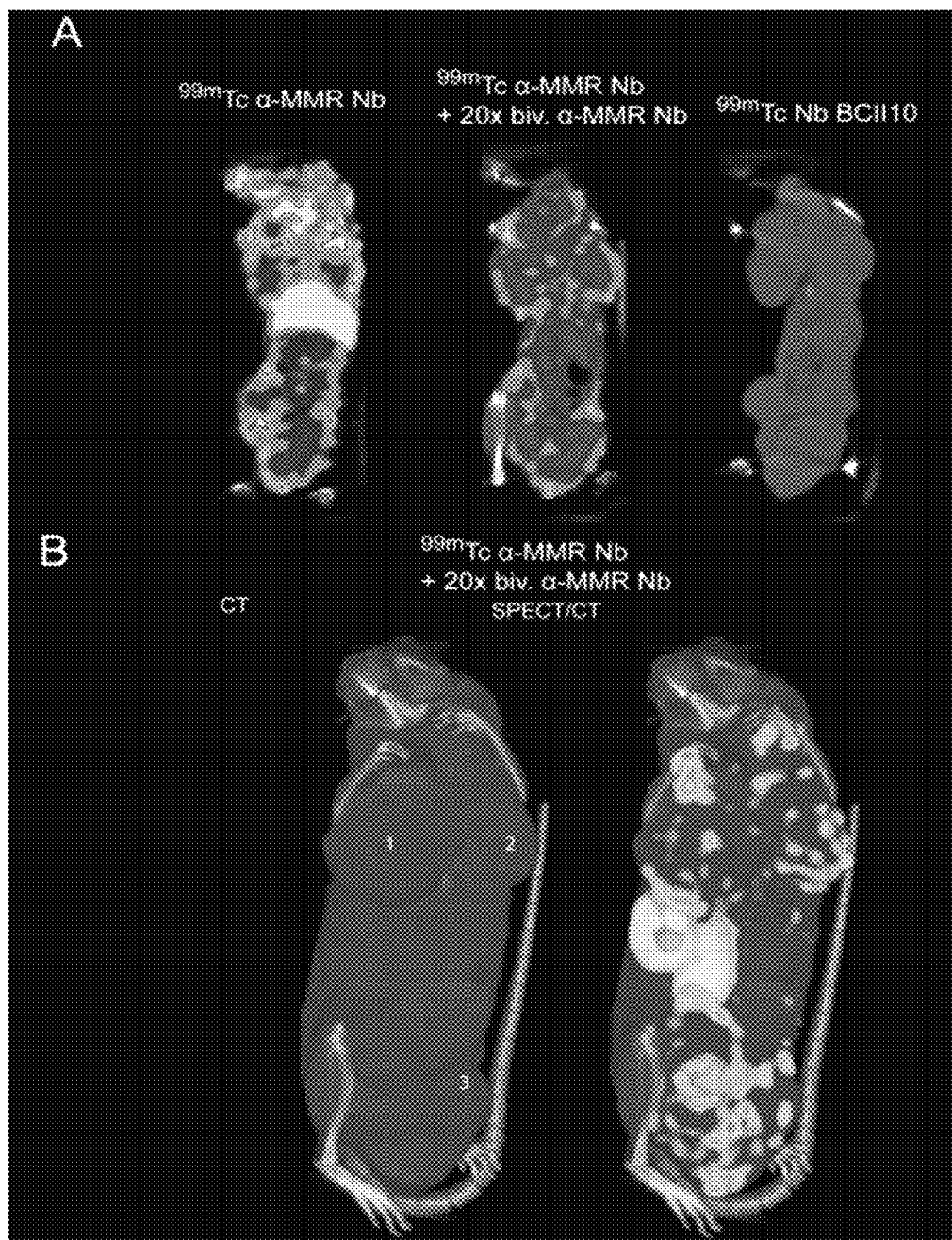


FIG. 27 (continued)

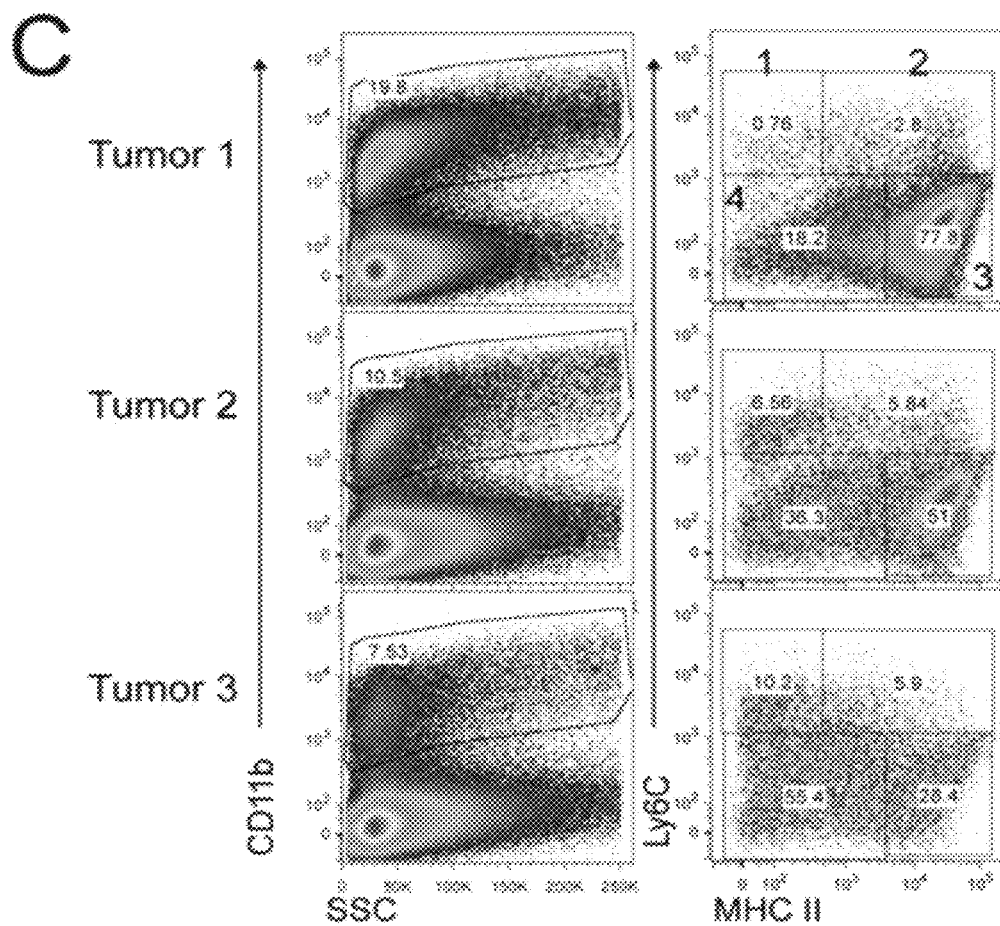


FIG. 27 (continued)

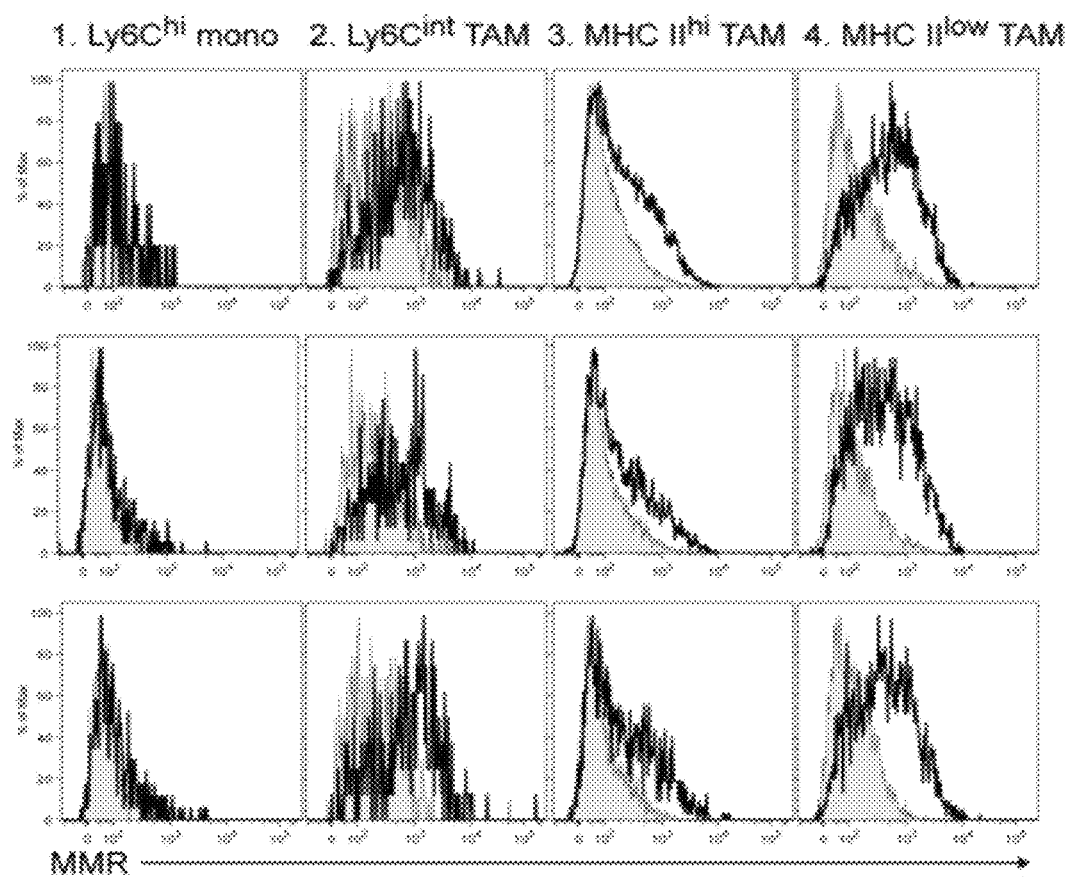


Figure 28

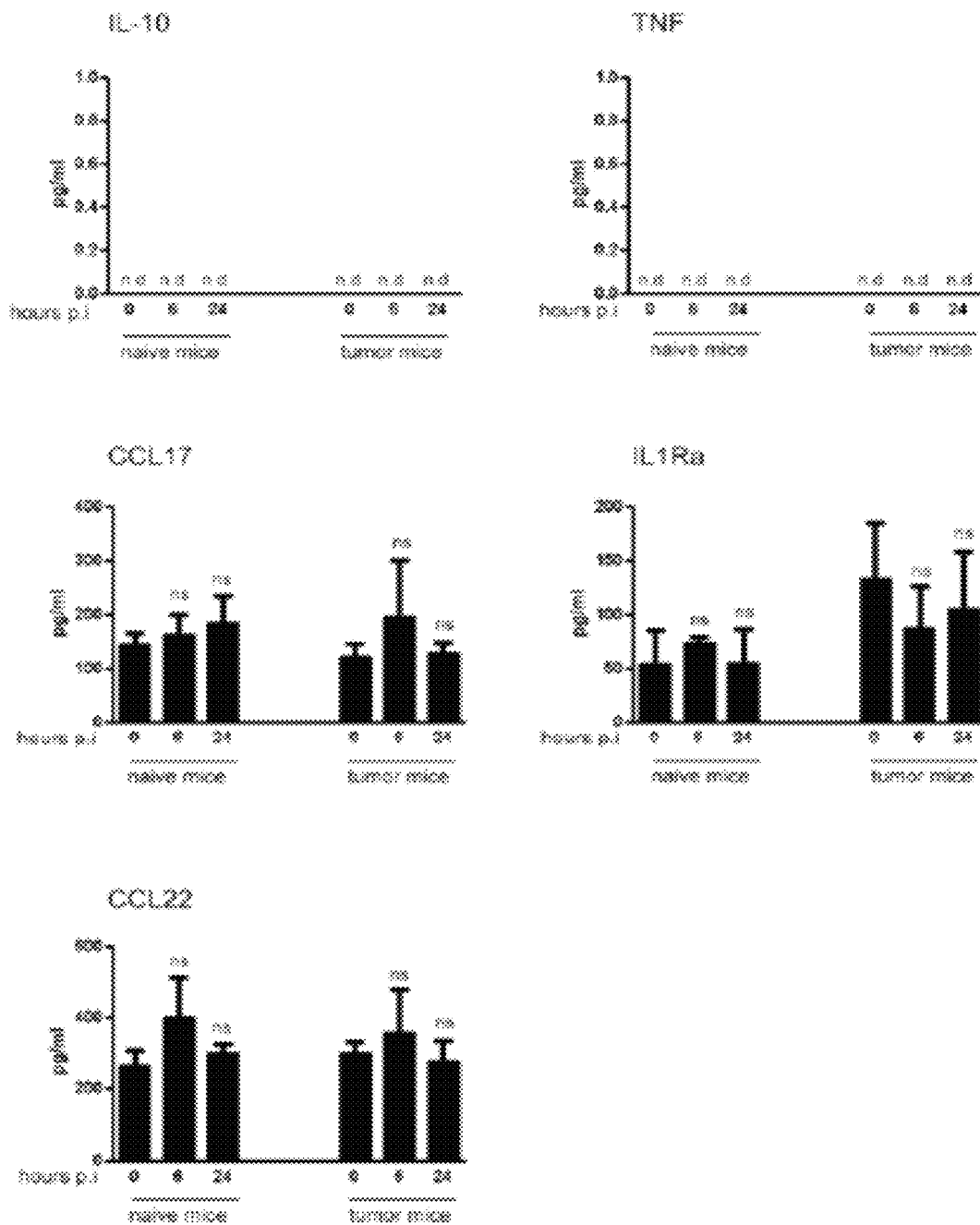


Figure 29

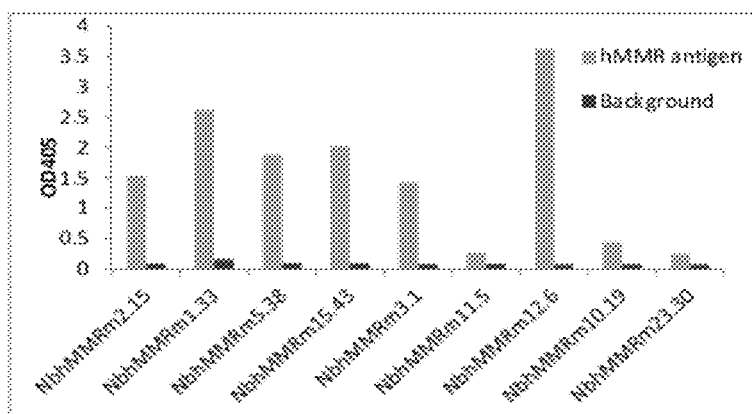


Figure 30

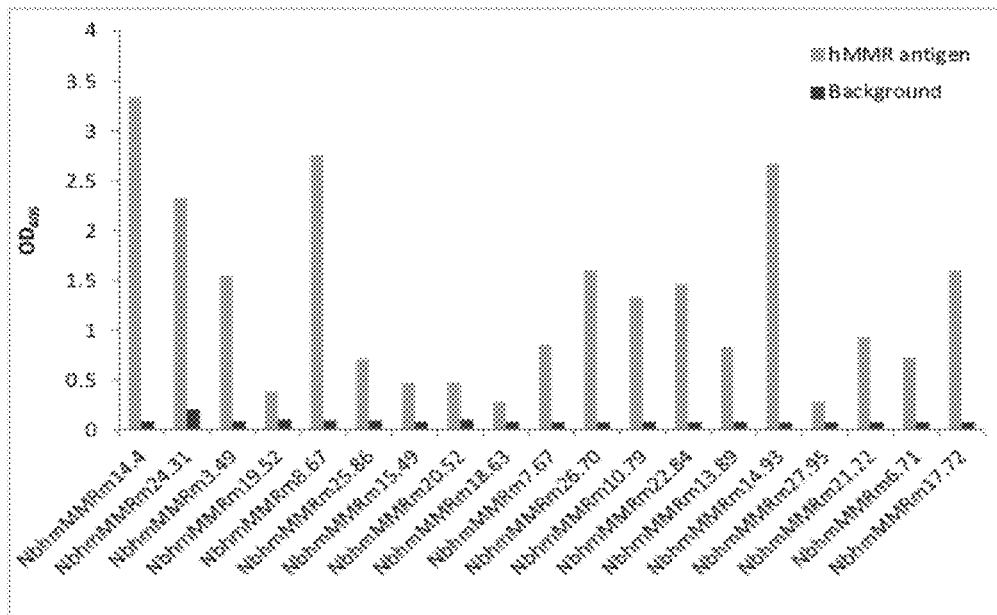
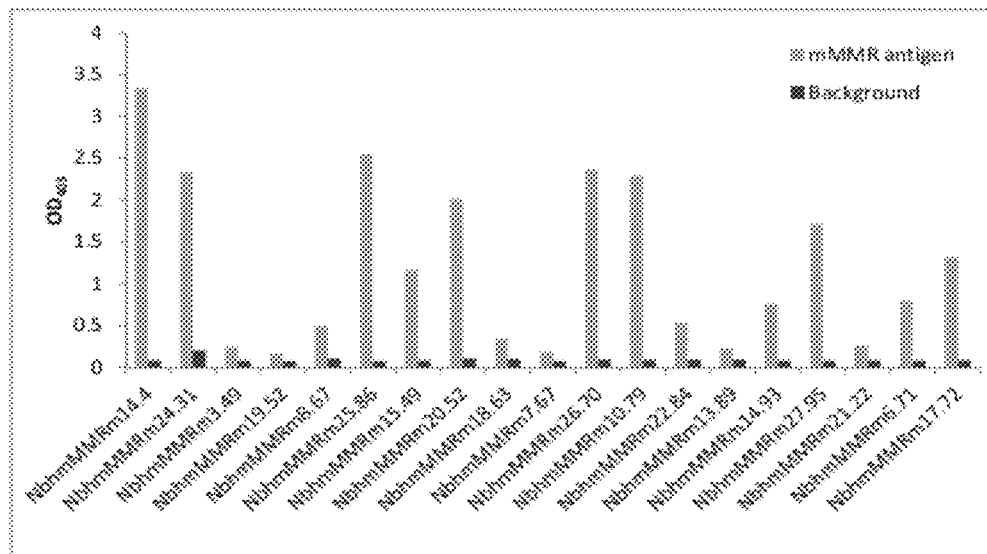


Figure 31



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**TARGETING AND IN VIVO IMAGING OF
TUMOR-ASSOCIATED MACROPHAGES****CROSS-REFERENCE TO RELATED
APPLICATION**

This application is a continuation-in-part of U.S. patent application Ser. No. 13/065,794 filed Mar. 29, 2011, which claims the benefit of U.S. Provisional Patent Application Ser. No. 61/341,356, filed Mar. 29, 2010, the disclosure of each of which is hereby incorporated herein in its entirety by this reference.

**STATEMENT ACCORDING TO 37 C.F.R.
§1.821(c) OR (e)—SEQUENCE LISTING
SUBMITTED AS ASCII TEXT FILE**

Pursuant to 37 C.F.R. §1.821(c) or (e), a file containing an ASCII text version of the Sequence Listing has been submitted concomitant with this application, the contents of which are hereby incorporated by reference.

FIELD OF THE INVENTION

The present invention relates to the field of tumor growth and biology. The invention relates to activities and characteristics of tumor-associated macrophages (TAMs). In particular, immunoglobulin single variable domains are provided against markers of TAMs, and methods using the same for in vivo imaging of tumor cells, as well as cancer diagnostics and therapeutics.

BACKGROUND

Tumors harbor dynamic microenvironments in which cancer cells are intimately associated with non-transformed host cells. The tumor-associated stroma is considered to play an important role during tumor growth, influencing phenomena such as angiogenesis, metastasis and immune suppression.⁽³⁶⁾ As such, the stroma forms an attractive target for diagnostic and therapeutic applications.⁽³⁷⁾

Different myeloid cells are important components of the tumor stroma. Myeloid cells are frequently found to infiltrate tumors and have been linked to diverse tumor-promoting activities.⁽⁴¹⁾ In particular, tumor-associated macrophages (TAMs) are an important component of the tumor stroma, both in murine models and human patients.⁽²⁾ TAMs can promote tumor-growth by affecting angiogenesis, immune suppression and invasion and metastasis.^(2,3)

Tissue-resident macrophages can be maintained through local proliferation or differentiation in situ from circulating monocytic precursors.⁽⁵⁾ Importantly, discrete subsets of blood monocytes have been described. Mouse monocytes can be classified as Ly6C^{low}CX₃CR1^{hi}(CCR2⁻CD62L⁻) or Ly6C^{hi}CX₃CR1^{low}(CCR2⁺CD62L⁺) and are shown to have distinct functions and migration patterns.⁽⁶⁾

Macrophages are plastic cells that can adopt different phenotypes depending on the immune context. Microenvironmental stimuli can drive a macrophage either towards a “classical” (M1) or an “alternative” (M2) activation state, two extremes in a spectrum.⁽⁷⁾ M1 macrophages are typically characterized by the expression of pro-inflammatory cytokines, inducible nitric oxide synthase 2 (Nos2) and MHC Class II molecules. M2 macrophages, have a decreased level of the aforementioned molecules and are identified by their signature-expression of a variety of markers, including arginase-1

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and mannose and scavenger receptors. It has been suggested that TAMs display a M2-like phenotype.⁽⁸⁾

Despite the presence of TAM in tumor infiltrate and their potential to produce angiogenic factors, their role in tumor growth and development remains unclear. There remains a need to discover and understand the complexities of the tumor-infiltrating myeloid cell compartment in view of the selective treatment of tumor growth.

SUMMARY OF THE INVENTION

Antibody-based tumor targeting strategies are widely explored.⁽³⁸⁾ Antibodies can be used for tumor imaging or delivering therapeutics to tumor cells. However, limitations of conventional antibodies include a poor penetration of solid tumors and high Fc-mediated aspecific binding, highlighting the need for smaller and more specific binding units. Further to that, antibody-based tumor-targeting approaches have mostly been directed against antigens expressed on cancer cells.⁽³⁸⁾ However, the antigenic profile of cancer cells can be unstable and depends on the cancer type. Tumors also contain a large stromal compartment, which includes myeloid cells such as macrophages.⁽³⁹⁾ Stromal cells might provide a good alternative for tumor-targeting, since their antigenic profile is more stable and might be similar across different cancer types.

The present invention is based on the inventor's surprising finding of the existence of molecularly and functionally distinct TAM subsets, located in different intratumoral regions and the unraveling of Ly6C^{hi} monocytes as their precursors. In particular, molecular markers for discriminating between these different TAM subsets, and accordingly, between these different intratumoral microenvironments (hypoxic versus normoxic zones), form the basis of the present invention. The present invention relates to the use of these molecular markers for specifically targeting the M1/M2-like or hypoxic/perivascular TAM subsets or their precursors, or, in a preferred embodiment, for selectively targeting the hypoxic/perivascular cells inside a tumor. The invention further relates to combinatorial strategies for optimally “re-educating” the TAM compartment and reverting its tumor-promoting activities.

In particular, selective in vivo targeting and imaging of distinct TAM subpopulations in the tumor stroma is envisaged by making use of specific immunoglobulin single variable domains, including nanobodies, against the corresponding molecular markers. Furthermore, a strategy was developed to reduce extra-tumoral signals to background levels, while persevering an efficient targeting of the tumor. Evidence is provided that TAM subsets can be efficiently targeted in vivo using nanobodies against the macrophage mannose receptor (MMR) in preclinical models, as illustrated in murine models. Moreover, evidence is provided that MMR⁺ TAMs can be detected in intratumoral hypoxic zones of human samples, as illustrated in human breast cancer samples.

Thus, the invention encompasses novel diagnostic, prognostic and therapeutic applications for the diagnosis and treatment of cancer based on the existence of distinct TAM subsets, corresponding molecular markers and targeting tools, and a selective tumor targeting methodology.

Objects of the present invention will be clear from the description that follows.

BRIEF DESCRIPTION OF THE DRAWINGS

The patent or application file contains at least one drawing executed in color. Copies of this patent or patent application

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publication with color drawing(s) will be provided by the Office upon request and payment of the necessary fee.

FIG. 1: TS/A tumors are infiltrated by distinct granulocyte and monocyte/macrophage subsets. (A) Single-cell suspensions of 11-day-old tumors were stained for the indicated markers. On gated CD11b⁺ cells, Ly6C was plotted vs. MHC II, demonstrating at least seven distinct subsets. For each subset, forward scatter (FSC) vs. side scatter (SSC) plots are shown. (B) Staining single-cell suspensions from 7-, 11-, 14- and 21-day-old tumors. Plots are gated on CD11b⁺ cells. Accompanying mean tumor diameters \pm SEM are indicated. n=3 experiments. (C) The expression of the indicated markers was assessed on cells present in gates 1-4, as shown in panel A. All markers were analyzed using antibody staining, except for CX3CR1, for which tumors were grown in CX3CR1GFP/+ mice. Shaded histograms are isotype controls or, for CX3CR1, autofluorescence in WT mice.

FIG. 2: Infiltration of latex-labeled monocytes in tumors and kinetics of BrdU incorporation in the distinct TAM subsets. (A) Six-day-old tumors were collected from control mice or mice in which the Ly6Clow or Ly6Chi monocytes were labeled. Plots are gated on CD11b⁺ cells. n=3 experiments. (B1) 6-, 12- or 19-day-old tumors were collected from untreated mice (control) or mice in which the Ly6Chi monocytes were labeled (latex injected). Plots are gated on CD11b⁺ cells. (B2) Ly6C vs. MHC II plots of tumor single-cell suspensions from latex injected mice at 6, 12 or 19 days p.i., either gated on the total CD11b⁺ population or on the latex+CD11b⁺ population. n=3 experiments. (C) Two weeks tumor-bearing mice were left untreated (0 hours) or continuously given BrdU for the indicated time, after which BrdU incorporation in tumor cells was measured. C1 shows how BrdU⁺ cells were gated in the different TAM subsets. n=2 BrdU-kinetic experiments (D) The intracellular expression of Ki67 was assessed via flow cytometry. Shaded histograms are isotype controls. n>3.

FIG. 3: Arginase, TNF α , and iNOS protein expression in MHC II^{hi} and MHC II^{low} TAMs. (A) Arginase enzymatic activity (mU) was measured in lysates of sorted TAMs. Values are the mean \pm SEM of three experiments. * p<0.05 (B) TNF α production by TAMs was measured using intracellular FACS. Bar diagrams represent the mean percentage TNF α + TAMs \pm SEM from three experiments. * p<0.05 (C) TAMs were left untreated or stimulated with IFN γ , LPS or LPS+ IFN γ for 12 hours. Subsequently, iNOS expression was evaluated using intracellular FACS. The percentage iNOS+ cells is shown as normalized Δ MFI (see Materials & Methods). n=2 experiments.

FIG. 4: MHC II^{low} TAMs are enriched in hypoxic regions, while MHC II^{hi} TAMs are mainly normoxic. (A) Three weeks tumor-bearing mice were injected with pimonidazole (HP-1). Frozen tumor sections were stained with MECA32 and anti-HP-1 antibodies and DAPI. (B) Frozen tumor sections from HP-1 injected mice were stained for CD11b, MHC II, HP-1 adducts and DAPI. (C) Assessment of HP-1 adducts in the distinct tumor myeloid subsets using FACS. n=4 experiments.

FIG. 5: Differential functions of TAM subsets. (A) Sorted TAMs were grafted on the developing chorioallantoic membrane from fertilized chicken eggs. BSA and rhVEGF grafting were used as negative and positive controls, respectively. At day 13, the number of vessels growing towards the implants was quantified. Values are the mean number of implant-directed vessels \pm SEM of eight individual eggs/condition of two experiments. * p<0.05; ** p<0.01. (B) Sorted TAM subsets or splenic Balb/c cDCs were cultured in the presence of purified C57BL/6 CD4⁺ or CD8⁺ T cells and

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T-cell proliferation was assessed. Graphs represent the average level of 3H-thymidine incorporation, expressed as Counts Per Minute (CPM), \pm SEM. n=3 experiments. (C) Sorted TAM subsets or splenic Balb/c cDC were added to naive Balb/c splenocytes. Co-cultures were stimulated with anti-CD3 and proliferation was assessed. n=3 experiments. (D) TAM subsets and Balb/c splenocytes were cultured at a 1:4 ratio and treated with anti-CD3 with or without the indicated inhibitors. Values represent the mean \pm SD of the relative percentage suppression taken over three experiments. * p<0.05

FIG. 6: Identifying Ly6C^{hi} and Ly6C^{low} monocytes in tumors. Eleven-day-old tumors were collected from CX₃CR1^{GFP/+} reporter mice. Within the gated CD11b⁺ population, Ly6C^{hi}MHC II⁻ and Ly6C^{low}MHC II⁻ cells were sub-gated and their respective CX₃CR1 vs. CCR3 plots are shown. Ly6C^{hi}MHC II⁻ cells were CCR3-CX₃CR1^{low} (Gate 1). Ly6C^{low}MHC II⁻ cells could be subdivided in CCR3⁻CX₃CR1^{low} (Gate 2), CCR3-CX₃CR1^{hi} (Gate 3) and CCR3⁺CX₃CR1⁻ cells (Gate E, comprising of eosinophils). Forward vs. Side Scatter plots for the distinct gates are shown in the bottom panel. Similar results were seen at different time points of tumor growth. For the indicated time point, results are representative of three independent experiments.

FIG. 7: Purities of sorted cell populations. Representative plots are shown of the FACS sorted cell populations that were used throughout the study. (A) MHC II^{hi} TAMs and MHC II^{low} TAMs (B) CD11c+MHC II^{hi}B220-Ly6C-splenic cDCs.

FIG. 8: Latex bead uptake by TAM subsets in vivo and in vitro. (A) Three weeks tumor-bearing mice were injected iv with fluorescent latex beads and 2 hours later, tumors were collected to assess latex uptake by the CD11b⁺ population. The depicted SSC vs. latex plot is on gated CD11b⁺ cells and shows how latex+ cells are gated. The percentage of Ly6Chi monocytes, Ly6Cint TAMs, MHC II^{hi} TAMs and MHC II^{low} TAMs within the total CD11b⁺ gate or CD11b+Latex+ gate is depicted for five individual groups of tumors from three independent experiments. (B) Tumor single cell suspensions were cultured in vitro, at 4 $^{\circ}$ C. or 37 $^{\circ}$ C., in the absence (control) or presence of latex beads for 40 minutes. Latex+ cells within the CD11b⁺ population were gated and their percentages are given. The percentage of the distinct monocyte/TAM subsets within the total CD11b⁺ gate or CD11b+Latex+ gate is depicted for five individual groups of tumors from three independent experiments for cells cultured at 37 $^{\circ}$ C.

FIG. 9: DQ-OVA processing by TAM subsets. TAMs were allowed to phagocytose and process DQ-OVA for 15 minutes at 0 $^{\circ}$ C. or 37 $^{\circ}$ C. Free DQ-OVA was subsequently removed from the culture medium and TAMs were given an additional 15, 30 and 60 minutes to process internalized DQ-OVA. DQ-OVA processing results in the formation of fluorescent peptides and fluorescence intensities for the gated TAM subsets are shown in histogram plots. Values are the mean percentage cells within the indicated gate \pm SEM from three independent experiments. p-values were calculated for these means between MHC II^{hi} vs. MHC II^{low} TAMs for each time point. * p<0.05

FIG. 10: Schematic summary.

FIG. 11: Biodistribution MMR Nb in naïve and knockout mice.

FIG. 12: Uptake experiments of MMR Nb in TS/A tumor-bearing mice.

FIG. 13: TAM subsets in the Lewis Lung Carcinoma (LLC) model and in the mammary carcinoma model 4T1.

FIG. 14: MMR expression on distinct cell types present in TS/A tumor suspensions. Single cell suspensions were made from TS/A tumors and MMR expression was evaluated on the

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indicated cell populations using an anti-MMR monoclonal antibody. Shaded histograms represent isotype control.

FIG. 15. Anti-MMR clone 1 differentially labels TAM subsets in TS/A tumor sections. TS/A tumors were collected from three weeks tumor-bearing mice and frozen sections were triple-stained for MMR (red), MHC II (green) and CD11b (blue).

FIG. 16. anti-MMR Nb differentially binds to TAM subsets in tumor single cell suspensions. (A) Single-cell suspensions of 21-day old TS/A tumors were stained with the indicated markers. anti-BCII10 Nb served as negative control. (B) Staining of anti-MMR Nb clone 1 was examined on the gated myeloid subsets. Shaded histograms represents staining with anti-BCII10 Nb.

FIG. 17. Coronal and sagittal views of fused Pinhole SPECT and Micro-CT images of naive WT or MMR^{-/-} mice 1 hour after injection with ^{99m}Tc labeled anti-MMR Nb clone 1. (A) In WT mice anti-MMR Nb shows kidney/bladder elimination and uptake in several organs. (B) In MMR^{-/-} mice anti-MMR Nb shows primarily kidney/bladder elimination.

FIG. 18. Coronal and transverse views of fused Pinhole SPECT and Micro-CT images of WT TS/A tumor-bearing mice 3 hours after injection with ^{99m}Tc labeled cAbBCII10 or anti-MMR Nb.

FIG. 19. Coronal and transverse views of fused Pinhole SPECT and Micro-CT images of WT and MMR^{-/-} 3LL tumor-bearing mice 3 hours after injection with ^{99m}Tc labeled cAbBCII10 or anti-MMR Nb.

FIG. 20. Uptake values of ^{99m}Tc-labeled monovalent anti-MMR Nb clone 1 in TS/A tumor-bearing mice upon co-injection with an eighty-fold excess of cold monovalent anti-MMR Nb, based on dissection at 3 hours post injection. Tracer uptake is expressed as injected activity per gram (% IA/g).

FIG. 21. Uptake values of ^{99m}Tc-labeled monovalent anti-MMR Nb clone 1 in TS/A tumor-bearing mice upon co-injection with a twenty-fold excess of cold bivalent anti-MMR Nb, based on dissection at 3 hours post injection. Tracer uptake is expressed as injected activity per gram (% IA/g).

FIG. 22. The relative abundance of TAM subsets is different in fast growing 3LL-R versus slow growing 3LL-S tumors. 3×10⁶ cancer cells were injected in the flank and tumor volumes were measured at different time intervals. When tumors reached a volume of about 1000 mm³, tumor single cell suspensions were made and the presence of TAM subsets were assessed via FACS.

FIG. 23. MHC II^{hi} TAM are located outside of hypoxic regions in 3LL-R tumors. 3LL-R tumors were collected from 12-days tumor-bearing mice and frozen sections were double-stained for MHC II (green) and Hypoxypore (blue). Pictures are shown from three distinct regions within the same tumor.

FIG. 24. α -MMR Nb targeting in WT and CCR2-KO tumor-bearing mice. (A) Percentages of MHC II^{low} TAMs and Ly6G⁺ neutrophils in tumor single-cell suspensions of WT and CCR2-KO tumors. Mean±SEM (n=4) (B) Uptake values of ^{99m}Tc-labeled α -MMR Nb c11 or Nb BCII10 in WT or CCR2-KO mice 12 days post 3LL-R injection. ***p<0.001 (C) AF647-labeled α -MMR Nb c11 and pimonidazole were injected i.v. in 3LL-R WT or MMR-KO tumor-bearers. Two hours later, tumors were collected and stained for F4/80 and hypoxypore. (D) Overlays of α -MMR Nb-AF647, hypoxypore and F4/80 signals in WT 3LL-R tumors.

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FIG. 25. Increasing tumor-to-tissue ratios of ^{99m}Tc- α -MMR Nb tracer uptake by excess unlabeled bivalent α -MMR Nb c11. (A) Overview of different Nb constructs. (B) Mono and bivalent ^{99m}Tc-labeled Nbs were injected in s.c. TS/A or 3LL-R tumor-bearing mice and uptake values were calculated 3 hours post injection via organ dissection (C) s.c. TS/A tumor-bearing mice were injected with ^{99m}Tc-labeled Nb BCII10, ^{99m}Tc-labeled α -MMR Nb c11 or ^{99m}Tc-labeled α -MMR Nb+twenty-fold molar excess of unlabeled bivalent α -MMR Nb c11. C1: uptake values of ^{99m}Tc- α -MMR Nb (expressed as injected activity per gram (% IA/g)) at 3 hours post injection. Mean±SEM (n=6). C2: α -MMR Nb-to-background ratio, calculated as ^{99m}Tc- α -MMR Nb uptake values/^{99m}Tc-Nb BCII10. C3: tumor-to-tissue ratio of ^{99m}Tc- α -MMR Nb, calculated as “tracer uptake in the tumor”/“tracer uptake in the organ.” Statistical significance was tested between ^{99m}Tc- α -MMR Nb and ^{99m}Tc- α -MMR Nb+cold Nb *p<0.05, **p<0.01, ***p<0.001.

FIG. 26. Fused Pinhole SPECT/Micro-CT images of mice co-injected with ^{99m}Tc-labeled α -MMR Nb with excess unlabeled bivalent α -MMR Nb. (A) Coronal views of subcutaneous TS/A-bearing mice 3 hours after injection of ^{99m}Tc-labeled α -MMR Nb c11, ^{99m}Tc-labeled α -MMR Nb c11+twenty-fold molar excess of unlabeled bivalent α -MMR Nb c11 or ^{99m}Tc-labeled Nb BCII10. (B) 3D reconstruction of SPECT/CT images of a subcutaneous TS/A-bearing mouse injected with indicated tracer, 3 hours p.i. (planar view; Video 1 for 3D view: data not shown) (C) Coronal and sagittal views of mice bearing orthotopic TS/A tumors in the mammary gland 3 hours after injection with indicated tracers. (D) High-resolution 3D reconstruction of CT and SPECT/CT images of an orthotopic TS/A-bearing mouse injected with indicated tracer, 3 hours p.i. (planar view; Video 2 for 3D view: data not shown).

FIG. 27. α -MMR Nb-based imaging and TAM targeting in MMTV-PyMT mice. (A) A MMTV-PyMT mouse with multiple macroscopic nodules was consecutively (48- to 76-hour intervals) injected with indicated tracers; images were taken 3 hours p.i. Coronal views are shown. n=3 (B) High-resolution 3D reconstruction of CT and SPECT/CT images of the same mouse after injection of ^{99m}Tc-labeled α -MMR Nb and blocking bivalent α -MMR Nb. Out of multiple nodules, the numbers indicate those tumors that were chosen for dissection (C) FACS analysis of single-cell suspensions from the tumors indicated in (B).

FIG. 28. Effect of mono- and bivalent α -MMR Nb on immune cell activation in vivo. To assess whether Nbs elicit a functional response in vivo, naive mice and 13 days 3LL-R tumor-bearing mice were left untreated or were stimulated (i.v. injection) with 5 μ g monovalent Nb+200 μ g bivalent Nb for 6 or 24 hours. Cytokine and chemokine production was assessed by sandwich ELISA on blood serum. Values are the mean±SEM of three experiments.

FIG. 29. PE-ELISA on human MMR. Summary of the selected anti-human MMR Nb clones. A clone was selected when the OD405 nm was at least three times higher on specific antigen as compared to irrelevant milk-blocking proteins.

FIG. 30. PE-ELISA on human MMR. Summary of the selected anti-human/mouse MMR cross-reactive Nb clones. A clone was selected when the OD405 nm was at least three times higher on specific antigen as compared to irrelevant milk-blocking proteins.

FIG. 31. PE-ELISA on mouse MMR. Summary of the selected anti-human/mouse MMR cross-reactive Nb clones.

A clone was selected when the OD₄₀₅ nm was at least two times higher on specific antigen as compared to irrelevant milk-blocking proteins.

DETAILED DESCRIPTION OF THE INVENTION

The present invention will be described with respect to particular embodiments and with reference to certain drawings but the invention is not limited thereto but only by the claims. Any reference signs in the claims shall not be construed as limiting the scope. The drawings described are only schematic and are non-limiting. In the drawings, the size of some of the elements may be exaggerated and not drawn on scale for illustrative purposes. Where the term "comprising" is used in the present description and claims, it does not exclude other elements or steps. Where an indefinite or definite article is used when referring to a singular noun e.g., "a" or "an," "the," this includes a plural of that noun unless something else is specifically stated. Furthermore, the terms first, second, third and the like in the description and in the claims, are used for distinguishing between similar elements and not necessarily for describing a sequential or chronological order. It is to be understood that the terms so used are interchangeable under appropriate circumstances and that the embodiments of the invention described herein are capable of operation in other sequences than described or illustrated herein.

Unless otherwise defined herein, scientific and technical terms and phrases used in connection with the present invention shall have the meanings that are commonly understood by those of ordinary skill in the art. Generally, nomenclatures used in connection with, and techniques of molecular and cellular biology, genetics and protein and nucleic acid chemistry and hybridization described herein are those well known and commonly used in the art. The methods and techniques of the present invention are generally performed according to conventional methods well known in the art and as described in various general and more specific references that are cited and discussed throughout the present specification unless otherwise indicated. See, for example, Sambrook et al. *Molecular Cloning: A Laboratory Manual*, 2d ed., Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y. (1989); Ausubel et al., *Current Protocols in Molecular Biology*, Greene Publishing Associates (1992, and Supplements to 2002).

As used herein, the terms "polypeptide," "protein," "peptide" are used interchangeably herein, and refer to a polymeric form of amino acids of any length, which can include coded and non-coded amino acids, chemically or biochemically modified or derivatized amino acids, and polypeptides having modified peptide backbones.

As used herein, the terms "nucleic acid molecule," "polynucleotide," "polynucleic acid," "nucleic acid" are used interchangeably and refer to a polymeric form of nucleotides of any length, either deoxyribonucleotides or ribonucleotides, or analogs thereof. Polynucleotides may have any three-dimensional structure, and may perform any function, known or unknown. Non-limiting examples of polynucleotides include a gene, a gene fragment, exons, introns, messenger RNA (mRNA), transfer RNA, ribosomal RNA, ribozymes, cDNA, recombinant polynucleotides, branched polynucleotides, plasmids, vectors, isolated DNA of any sequence, control regions, isolated RNA of any sequence, nucleic acid probes, and primers. The nucleic acid molecule may be linear or circular.

A first aspect of the invention relates to an immunoglobulin single variable domain directed against and/or specifically binding to a molecular marker of Table 1.

According to a particular embodiment, the invention relates to an immunoglobulin single variable domain that is directed against and/or specifically binds to the macrophage mannose receptor. The immunoglobulin single variable domains of the present invention may generally be directed against any MMR, in particular a mammalian macrophage mannose receptor, and in particular mouse macrophage mannose receptor (SEQ ID NO:260) and/or human macrophage mannose receptor (SEQ ID NO:258). The present invention is in its broadest sense not particularly limited to or defined by a specific antigenic determinant, epitope, part, domain, subunit or conformation of MMR, and in particular mouse MMR (SEQ ID NO:260) and/or human macrophage mannose receptor (SEQ ID NO:258) against which the immunoglobulin single variable domains are directed. According to a specific preferred embodiment, the immunoglobulin single variable domain specifically binds to the ectodomain of the macrophage mannose receptor, and in particular the ectodomain of the mouse macrophage mannose receptor (SEQ ID NO:263) and/or the ectodomain of the human macrophage mannose receptor (SEQ ID NO:262).

The "macrophage mannose receptor" (MMR), as used herein, refers to a type I transmembrane protein, first identified in mammalian tissue macrophages and later in dendritic cells and a variety of endothelial and epithelial cells. Macrophages are central actors of the innate and adaptive immune responses. They are disseminated throughout most organs to protect against entry of infectious agents by internalizing and most of the time, killing them. Among the surface receptors present on macrophages, the mannose receptor recognizes a variety of molecular patterns generic to microorganisms. The MMR is composed of a single subunit with N- and O-linked glycosylations and consists of five domains: an N-terminal cysteine-rich region, which recognizes terminal sulfated sugar residues; a fibronectin type II domain with unclear function; a series of eight C-type, lectin-like carbohydrate recognition domains (CRDs) involved in Ca²⁺-dependent recognition of mannose, fucose, or N-acetylglucosamine residues on the envelop of pathogens or on endogenous glycoproteins with CRDs 4-8 showing affinity for ligands comparable with that of intact MR; a single transmembrane domain; and a 45 residue-long cytoplasmic tail that contains motifs critical for MR-mediated endocytosis and sorting in endosomes.⁽⁴⁷⁾

Preferably, the macrophage mannose receptor is of mammalian origin, particularly from mouse, rat, human, and the like, and these cross-species variants of the MMR protein are referred to herein as "homologues" of the macrophage mannose receptor. Thus, the macrophage mannose receptor as referred to in the present invention includes homologues as well as fragments of the full-length MMR protein. Non-limiting examples of homologues of the MMR include the mouse MMR (synonyms: MRC1 or CD206; accession number nucleotide sequence: NM_008625.2; accession number protein sequence: NP_032651.2 and as in SEQ ID NO:260) or the human MMR (synonyms: MRC1 or CD206; accession number nucleotide sequence: NM_002438.2; accession number protein sequence: NP_002429.1 and as in SEQ ID NO:258). The deduced amino acid sequence of mouse mannose receptor has an overall 82% homology with the human mannose receptor, as can be easily measured in a BLASTp alignment.⁽⁵¹⁾ A non-limiting example of a fragment of the full-length MMR protein includes the ectodomain of a particular MMR. The "ectodomain" as used herein, refers to a

fragment of the MMR containing an N-terminus that is cysteine-rich, followed by a fibronectin type II domain and eight carbohydrate recognition domains (CRDs). All of the eight CRDs are particularly well conserved, especially CRD4. For example, mouse CRD4 shows 92% homology with the equivalent region of the human protein. The ectodomain of the mouse macrophage mannose receptor is defined as the AA 19-AA 1388 fragment (SEQ ID NO:263) of the corresponding full-length mouse MMR amino acid sequence as defined in NP_032651.2 (SEQ ID NO:260). Or, the ectodomain of the human macrophage mannose receptor is defined as the AA 19-AA 1383 fragment (SEQ ID NO:262) of the corresponding full-length mouse MMR amino acid sequence as defined in NP_002429.1 (SEQ ID NO:258), see also Table 15.

The present invention thus provides for an immunoglobulin single variable domain specifically recognizing a marker of Table 1, preferably the macrophage mannose receptor (as defined above). As used herein, the term “specifically recognizing” or “specifically binding to” or simply “specific for” refers to the ability of an immunoglobulin or an immunoglobulin fragment, such as an immunoglobulin single variable domain, to preferentially bind to a particular antigen that is present in a homogeneous mixture of different antigens and does not necessarily imply high affinity (as defined further herein). In certain embodiments, a specific binding interaction will discriminate between desirable and undesirable antigens in a sample, in some embodiments more than about 10- to 100-fold or more (e.g., more than about 1000- or 10,000-fold). The terms “specifically bind,” “selectively bind,” “preferentially bind,” and grammatical equivalents thereof, are used interchangeably herein.

The term “affinity,” as used herein, refers to the degree to which an immunoglobulin single variable domain, binds to an antigen so as to shift the equilibrium of antigen and immunoglobulin single variable domain toward the presence of a complex formed by their binding. Thus, for example, where an antigen and antibody (fragment) are combined in relatively equal concentration, an antibody (fragment) of high affinity will bind to the available antigen so as to shift the equilibrium toward high concentration of the resulting complex. The dissociation constant is commonly used to describe the affinity between the antibody (fragment) and the antigenic target. Typically, the dissociation constant is lower than 10^{-5} M. Preferably, the dissociation constant is lower than 10^{-6} M, more preferably, lower than 10^{-7} M. Most preferably, the dissociation constant is lower than 10^{-8} M.

An immunoglobulin single variable domain that can specifically bind to and/or that has affinity for a specific antigen or antigenic determinant (e.g., epitope) is said to be “against” or “directed against” the antigen or antigenic determinant. An immunoglobulin single variable domain according to the invention is said to be “cross-reactive” for two different antigens or antigenic determinants (such as macrophage mannose receptor from two different species of mammal, such as human MMR and mouse MMR) if it is specific for both these different antigens or antigenic determinants.

It will be appreciated that, according to the invention, immunoglobulin single variable domains that are directed against the macrophage mannose receptor from one species may or may not show cross-reactivity with the macrophage mannose receptor from another species. For example, immunoglobulin single variable domains directed against human MMR, in particular human MMR (SEQ ID NO:258) may or may not show cross-reactivity with MMR from one or more other species of animals that are often used in animal models for diseases (for example, mouse, rat, rabbit, pig or dog). It

will be clear to the skilled person that such cross-reactivity, when present, may have advantages for diagnostic and/or therapeutic development, since it allows the immunoglobulin single variable domains to be tested in such disease models. It is expected that the immunoglobulin single variable domains according to the invention will generally bind to all naturally occurring or synthetic analogs, variants, mutants, alleles of the MMRs mentioned herein.

As used herein, an “immunoglobulin single variable domain” is an antigen-binding domain or fragment that comprises an amino acid sequence that comprises four framework regions (FR) and three complementarity determining regions (CDR) according to the following formula (1):

$$\text{FR1-CDR1-FR2-CDR2-FR3-CDR3-FR4} \quad (1);$$

or any suitable fragment thereof (which will then usually contain at least some of the amino acid residues that form at least one of the complementarity determining regions), and in which FR1 to FR4 refer to framework regions 1 to 4, respectively, and in which CDR1 to CDR3 refer to the complementarity determining regions 1 to 3, respectively.

Immunoglobulin single variable domains comprising 4 FRs and 3 CDRs are known to the person skilled in the art and have been described, as a non-limiting example, in reference (40). Typical, but non-limiting, examples of immunoglobulin single variable domains include light chain variable domain sequences (e.g., a V_L domain sequence), or heavy chain variable domain sequences (e.g., a V_H domain sequence), which are usually derived from conventional four-chain antibodies. Preferably, the immunoglobulin single variable domains are derived from camelid antibodies, preferably from heavy chain camelid antibodies, devoid of light chains, and are known as V_HH domain sequences or nanobodies (as described further herein).

A nanobody (Nb) is the smallest functional fragment or single variable domain (V_HH) of a naturally occurring single-chain antibody and is known to the person skilled in the art. They are derived from heavy chain only antibodies, seen in camelids.^(26,27) In the family of “camelids” immunoglobulins devoid of light polypeptide chains are found. “Camelids” comprise old world camelids (*Camelus bactrianus* and *Camelus dromedarius*) and new world camelids (for example, *Lama paccos*, *Lama glama*, *Lama guanicoe* and *Lama vicugna*). The single variable domain heavy chain antibody is herein designated as a Nanobody or a V_HH antibody. Nanobody™, Nanobodies™ and Nanoclone™ are trademarks of Ablynx NV (Belgium). The small size and unique biophysical properties of Nbs excel conventional antibody fragments for the recognition of uncommon or hidden epitopes and for binding into cavities or active sites of protein targets. Further, Nbs can be designed as multi-specific and multivalent antibodies (as defined further herein) or attached to reporter molecules.⁽²⁸⁾ Nbs are stable, survive the gastro-intestinal system and can easily be manufactured. Therefore, Nbs can be used in many applications including drug discovery and therapy, but also as a versatile and valuable tool for purification, functional study and crystallization of proteins.⁽²⁹⁾

The nanobodies of the invention generally comprise a single amino acid chain that can be considered to comprise four “framework regions” or FRs and three “complementarity determining regions” or CDRs, according to formula (1) (as defined above). The term “complementarity determining region” or “CDR” refers to variable regions in nanobodies and contains the amino acid sequences capable of specifically binding to antigenic targets. These CDR regions account for the basic specificity of the nanobody for a particular antigenic determinant structure. Such regions are also referred to as

“hypervariable regions.” The nanobodies have three CDR regions, each non-contiguous with the others (termed CDR1, CDR2, CDR3). The delineation of the FR and CDR sequences is often based on the IMGT unique numbering system for V-domains and V-like domains.⁽³⁵⁾ Alternatively, the delineation of the FR and CDR sequences can be done by using the Kabat numbering system as applied to V_HH domains from Camelids in the article of Riechmann and Muyldermans.⁽⁴¹⁾ As will be known by the person skilled in the art, the nanobodies can in particular be characterized by the presence of one or more Camelidae hallmark residues in one or more of the framework sequences (according to Kabat numbering), as described, for example, in WO 08/020,079, on page 75, Table A-3, incorporated herein by reference).

Non-limiting examples of nanobodies according to the present invention are as described herein and include anti-human, anti-mouse and cross-reactive anti-human/anti-mouse MMR nanobodies. For example, in Table 4, in particular SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:112, SEQ ID NO:114, SEQ ID NO:116; in Table 14, in particular SEQ ID NOS:126-155). In a specific embodiment, the nanobodies of the present invention may comprise at least one of the complementarity determining regions (CDRs) as described herein, for example, CDRs with an amino acid sequence selected from SEQ ID NOS:156-251 (see Table 14). Preferably, the nanobodies of the present invention comprise a CDR1, a CDR2 and a CDR3 selected from the group consisting of SEQ ID NOS:156-251 according to the above described formula (1). More specifically, the nanobodies can be selected from the group comprising SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:112, SEQ ID NO:114, SEQ ID NO:116, SEQ ID NOS:126-155, or a functional fragment thereof. A “functional fragment” or a “suitable fragment,” as used herein, may, for example, comprise one of the CDR loops. Preferably, the functional fragment comprises CDR3. More specifically, the nanobodies consist of any of SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:112, SEQ ID NO:114, SEQ ID NO:116, or SEQ ID NOS:126-155. In still another embodiment, a nucleic acid sequence encoding any of the above nanobodies or functional fragments is also part of the present invention (for example, see Table 4; SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:111, SEQ ID NO:113, SEQ ID NO:115). Further, the present invention also envisages expression vectors comprising nucleic acid sequences encoding any of the above nanobodies or functional fragments thereof, as well as host cells expressing such expression vectors. Suitable expression systems include constitutive and inducible expression systems in bacteria or yeasts, virus expression systems, such as baculovirus, semliki forest virus and lentiviruses, or transient transfection in insect or mammalian cells. Suitable host cells include *E. coli*, *Lactococcus lactis*, *Saccharomyces cerevisiae*, *Schizosaccharomyces pombe*, *Pichia pastoris*, and the like. Suitable animal host cells include HEK 293, COS, S2, CHO, NSO, DT40 and the like. The cloning, expression and/or purification of the nanobodies can be done according to techniques known by the skilled person in the art. For the sake of clarity, it is expected that at least some of the nanobodies identified herein may also be cross-reactive with macrophage mannose receptors of other mammalian species.

It should be noted that the term nanobody as used herein in its broadest sense is not limited to a specific biological source or to a specific method of preparation. For example, the nanobodies of the invention can generally be obtained: (1) by isolating the V_HH domain of a naturally occurring heavy chain antibody; (2) by expression of a nucleotide sequence

encoding a naturally occurring V_HH domain; (3) by “humanization” of a naturally occurring V_HH domain or by expression of a nucleic acid encoding a such humanized V_HH domain; (4) by “camelization” of a naturally occurring VH domain from any animal species, and in particular from a mammalian species, such as from a human being, or by expression of a nucleic acid encoding such a camelized VH domain; (5) by “camelization” of a “domain antibody” or “Dab” as described in the art, or by expression of a nucleic acid encoding such a camelized VH domain; (6) by using synthetic or semi-synthetic techniques for preparing proteins, polypeptides or other amino acid sequences known per se; (7) by preparing a nucleic acid encoding a nanobody using techniques for nucleic acid synthesis known per se, followed by expression of the nucleic acid thus obtained; and/or (8) by any combination of one or more of the foregoing.

One preferred class of nanobodies corresponds to the V_HH domains of naturally occurring heavy chain antibodies directed against a macrophage mannose receptor. As further described herein, such V_HH sequences can generally be generated or obtained by suitably immunizing a species of Camelid with a MMR (i.e., so as to raise an immune response and/or heavy chain antibodies directed against a MMR), by obtaining a suitable biological sample from the Camelid (such as a blood sample, or any sample of B-cells), and by generating V_HH sequences directed against a MMR, starting from the sample, using any suitable technique known per se. Such techniques will be clear to the skilled person. Alternatively, such naturally occurring V_HH domains against MMR can be obtained from naive libraries of Camelid V_HH sequences, for example, by screening such a library using MMR or at least one part, fragment, antigenic determinant or epitope thereof using one or more screening techniques known per se. Such libraries and techniques are, for example, described in WO9937681, WO0190190, WO03025020 and WO03035694. Alternatively, improved synthetic or semi-synthetic libraries derived from naive V_HH libraries may be used, such as V_HH libraries obtained from naive V_HH libraries by techniques such as random mutagenesis and/or CDR shuffling, as, for example, described in WO0043507. Yet another technique for obtaining V_HH sequences directed against a MMR involves suitably immunizing a transgenic mammal that is capable of expressing heavy chain antibodies (i.e., so as to raise an immune response and/or heavy chain antibodies directed against a MMR), obtaining a suitable biological sample from the transgenic mammal (such as a blood sample, or any sample of B-cells), and then generating V_HH sequences directed against a MMR starting from the sample, using any suitable technique known per se. For example, for this purpose, the heavy chain antibody-expressing mice and the further methods and techniques described in WO02085945 and in WO04049794 can be used.

Accordingly, the invention encompasses methods of generating immunoglobulin single variable domains according to the invention. As a non-limiting example, a method is provided of generating nanobodies directed against or specifically binding to the macrophage mannose receptor (as described herein), comprising:

- (i) immunizing an animal with a MMR, in particular a mouse (SEQ ID NOS:260, 261, 263) or human MMR (SEQ ID NOS:258, 259, 262), or a fragment thereof; and
- (ii) screening for nanobodies specifically binding to the MMR.

For the immunization of an animal with a MMR, the MMR may be produced and purified using conventional methods that may employ expressing a recombinant form of the MMR in a host cell, and purifying the MMR using affinity chroma-

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tography and/or antibody-based methods. Any suitable animal, e.g., a warm-blooded animal, in particular a mammal such as a rabbit, mouse, rat, camel, sheep, cow, shark, or pig or a bird such as a chicken or turkey, may be immunized using any of the techniques well known in the art suitable for generating an immune response. The screening for nanobodies, as a non-limiting example, specifically binding to a MMR may, for example, be performed by screening a set, collection or library of cells that express heavy chain antibodies on their surface (e.g., B-cells obtained from a suitably immunized Camelid), or bacteriophages that display a fusion of genIII and nanobody at their surface, by screening of a (naïve or immune) library of V_HH sequences or nanobody sequences, or by screening of a (naïve or immune) library of nucleic acid sequences that encode VHH sequences or nanobody sequences, which may all be performed in a manner known per se, and which method may optionally further comprise one or more other suitable steps, such as, for example, and without limitation, a step of affinity maturation, a step of expressing the desired amino acid sequence, a step of screening for binding and/or for activity against the desired antigen (in this case, the MMR), a step of determining the desired amino acid sequence or nucleotide sequence, a step of introducing one or more humanizing substitutions, a step of formatting in a suitable multivalent and/or multispecific format, a step of screening for the desired biological and/or physiological properties (i.e., using a suitable assay known in the art), and/or any combination of one or more of such steps, in any suitable order.

A particularly preferred class of immunoglobulin single variable domains of the invention comprises nanobodies with an amino acid sequence that corresponds to the amino acid sequence of a naturally occurring V_HH domain, but that has been “humanized,” i.e., by replacing one or more amino acid residues in the amino acid sequence of the naturally occurring V_HH sequence (and in particular in the framework sequences) by one or more of the amino acid residues that occur at the corresponding position(s) in a VH domain from a conventional four-chain antibody from a human being. This can be performed in a manner known per se, which will be clear to the skilled person, on the basis of the further description herein and the prior art on humanization. Again, it should be noted that such humanized nanobodies of the invention can be obtained in any suitable manner known per se (i.e., as indicated under points (1)-(8) above) and thus are not strictly limited to polypeptides that have been obtained using a polypeptide that comprises a naturally occurring V_HH domain as a starting material. Humanized nanobodies may have several advantages, such as a reduced immunogenicity, compared to the corresponding naturally occurring V_HH domains. Such humanization generally involves replacing one or more amino acid residues in the sequence of a naturally occurring V_HH with the amino acid residues that occur at the same position in a human VH domain, such as a human VH3 domain. The humanizing substitutions should be chosen such that the resulting humanized nanobodies still retain the favorable properties of nanobodies as defined herein. The skilled person will be able to select humanizing substitutions or suitable combinations of humanizing substitutions which optimize or achieve a desired or suitable balance between the favorable properties provided by the humanizing substitutions on the one hand and the favorable properties of naturally occurring V_HH domains on the other hand.

For example, both “humanization” and “camelization” can be performed by providing a nucleotide sequence that encodes a naturally occurring V_HH domain or VH domain, respectively, and then changing, in a manner known per se,

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one or more codons in the nucleotide sequence in such a way that the new nucleotide sequence encodes a “humanized” or “camelized” nanobody of the invention, respectively. This nucleic acid can then be expressed in a manner known per se, so as to provide the desired nanobody of the invention. Alternatively, based on the amino acid sequence of a naturally occurring VHH domain or VH domain, respectively, the amino acid sequence of the desired humanized or camelized Nanobody of the invention, respectively, can be designed and then synthesized de novo using techniques for peptide synthesis known per se. Also, based on the amino acid sequence or nucleotide sequence of a naturally occurring V_HH domain or VH domain, respectively, a nucleotide sequence encoding the desired humanized or camelized Nanobody of the invention, respectively, can be designed and then synthesized de novo using techniques for nucleic acid synthesis known per se, after which the nucleic acid thus obtained can be expressed in a manner known per se, so as to provide the desired nanobody of the invention. Other suitable methods and techniques for obtaining the nanobodies of the invention and/or nucleic acids encoding the same, starting from naturally occurring VH sequences or preferably VHH sequences, will be clear from the skilled person, and may, for example, comprise combining one or more parts of one or more naturally occurring VH sequences (such as one or more FR sequences and/or CDR sequences), one or more parts of one or more naturally occurring V_HH sequences (such as one or more FR sequences or CDR sequences), and/or one or more synthetic or semi-synthetic sequences, in a suitable manner, so as to provide a nanobody of the invention or a nucleotide sequence or nucleic acid encoding the same.

Also within the scope of the invention are natural or synthetic analogs, mutants, variants, alleles, homologs and orthologs (herein collectively referred to as “variants”) of the immunoglobulin single variable domains of the invention as defined herein. Some particularly preferred, but non-limiting examples of immunoglobulin single variable domains, as well as combinations of CDR sequences are mentioned in Table 14, which lists the CDR sequences that are present in a number of preferred, but non-limiting immunoglobulin single variable domains of the invention. Thus, according to one embodiment of the invention, the term “immunoglobulin single variable domain of the invention” in its broadest sense also covers such variants, in particular variants of the nanobodies of SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:112, SEQ ID NO:114, SEQ ID NO:116, SEQ ID NOS:126-155 (see Table 4, Table 14). Generally, in such variants, one or more amino acid residues may have been replaced, deleted and/or added, compared to the nanobodies of the invention as defined herein. Such substitutions, insertions or deletions may be made in one or more of the framework regions and/or in one or more of the CDRs, and in particular variants of the CDRs of the nanobodies of SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:112, SEQ ID NO:114, SEQ ID NO:116, SEQ ID NOS:126-155, the CDRs corresponding to SEQ ID NOS:156-251 (Table 14). Variants, as used herein, are sequences wherein each or any framework region and each or any complementarity determining region shows at least 80% identity, preferably at least 85% identity, more preferably 90% identity, even more preferably 95% identity or, still even more preferably 99% identity with the corresponding region in the reference sequence (i.e., FR1_variant versus FR1_reference, CDR1_variant versus CDR1_reference, FR2_variant versus FR2_reference, CDR2_variant versus CDR2_reference, FR3_variant versus FR3_reference, CDR3_variant versus CDR3_reference, FR4_variant versus

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FR4_reference), as can be measured electronically by making use of algorithms such as PILEUP and BLAST.^(50,51) Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information (on the worldwide web at ncbi.nlm.nih.gov/). Such variants of immunoglobulin single variable domains may be of particular advantage since they may have improved potency or other desired properties.

A “deletion” is defined here as a change in either amino acid or nucleotide sequence in which one or more amino acid or nucleotide residues, respectively, are absent as compared to an amino acid sequence or nucleotide sequence of a parental polypeptide or nucleic acid. Within the context of a protein, a deletion can involve deletion of about two, about five, about ten, up to about twenty, up to about thirty or up to about fifty or more amino acids. A protein or a fragment thereof may contain more than one deletion.

An “insertion” or “addition” is that change in an amino acid or nucleotide sequences which has resulted in the addition of one or more amino acid or nucleotide residues, respectively, as compared to an amino acid sequence or nucleotide sequence of a parental protein. “Insertion” generally refers to addition to one or more amino acid residues within an amino acid sequence of a polypeptide, while “addition” can be an insertion or refer to amino acid residues added at an N- or C-terminus, or both termini. Within the context of a protein or a fragment thereof, an insertion or addition is usually of about one, about three, about five, about ten, up to about twenty, up to about thirty or up to about fifty or more amino acids. A protein or fragment thereof may contain more than one insertion.

A “substitution,” as used herein, results from the replacement of one or more amino acids or nucleotides by different amino acids or nucleotides, respectively as compared to an amino acid sequence or nucleotide sequence of a parental protein or a fragment thereof. It is understood that a protein or a fragment thereof may have conservative amino acid substitutions which have substantially no effect on the protein’s activity. By conservative substitutions is intended combinations such as gly, ala; val, ile, leu, met; asp, glu; asn, gln; ser, thr; lys, arg; cys, met; and phe, tyr, trp.

By means of non-limiting examples, a substitution may, for example, be a conservative substitution (as described herein) and/or an amino acid residue may be replaced by another amino acid residue that naturally occurs at the same position in another V_H/V_L domain. Thus, any one or more substitutions, deletions or insertions, or any combination thereof, that either improve the properties of the nanobody of the invention or that at least do not detract too much from the desired properties or from the balance or combination of desired properties of the nanobody of the invention (i.e., to the extent that the nanobody is no longer suited for its intended use) are included within the scope of the invention. A skilled person will generally be able to determine and select suitable substitutions, deletions or insertions, or suitable combinations of thereof, based on the disclosure herein and optionally after a limited degree of routine experimentation, which may, for example, involve introducing a limited number of possible substitutions and determining their influence on the properties of the nanobodies thus obtained.

According to particularly preferred embodiments, variants of the immunoglobulin single variable domains, in particular the nanobodies of the present invention may have a substitution, deletion or insertion, of one, two or three amino acids in one, two or three of the CDRs, more specifically (i) in CDR1 or CDR2 or CDR3; (ii) in CDR1 and CDR2, or, in CDR1 and CDR3, or, in CDR2 and CDR3; (iii) in CDR1 and CDR2 and

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CDR3, as listed in Table 14. More preferably, variants of the immunoglobulin single variable domains, in particular the nanobodies, of the present invention may have a conservative substitution (as defined herein) of one, two or three amino acids in one, two or three of the CDRs, more specifically (i) in CDR1 or CDR2 or CDR3; (ii) in CDR1 and CDR2, or, in CDR1 and CDR3, or, in CDR2 and CDR3; (iii) in CDR1 and CDR2 and CDR3, as listed in Table 14.

Further, depending on the host organism used to express the immunoglobulin single variable domain of the invention, such deletions and/or substitutions may be designed in such a way that one or more sites for post-translational modification (such as one or more glycosylation sites) are removed, as will be within the ability of the person skilled in the art. Alternatively, substitutions or insertions may be designed so as to introduce one or more sites for attachment of functional groups (as described herein), for example, to allow site-specific pegylation.

Examples of modifications, as well as examples of amino acid residues within the immunoglobulin single variable domain, preferably the nanobody sequence, that can be modified (i.e., either on the protein backbone but preferably on a side chain), methods and techniques that can be used to introduce such modifications and the potential uses and advantages of such modifications will be clear to the skilled person. For example, such a modification may involve the introduction (e.g., by covalent linking or in another suitable manner) of one or more functional groups, residues or moieties into or onto the immunoglobulin single variable domain of the invention, and in particular of one or more functional groups, residues or moieties that confer one or more desired properties or functionalities to the immunoglobulin single variable domain of the invention. Examples of such functional groups and of techniques for introducing them will be clear to the skilled person, and can generally comprise all functional groups and techniques mentioned in the general background art cited hereinabove as well as the functional groups and techniques known per se for the modification of pharmaceutical proteins, and in particular for the modification of antibodies or antibody fragments (including ScFvs and single domain antibodies), for which reference is, for example, made to *Remington’s Pharmaceutical Sciences*, 16th ed., Mack Publishing Co., Easton, Pa. (1980). Such functional groups may, for example, be linked directly (for example, covalently) to a immunoglobulin single variable domain of the invention, or optionally via a suitable linker or spacer, as will again be clear to the skilled person. One of the most widely used techniques for increasing the half-life and/or reducing immunogenicity of pharmaceutical proteins comprises attachment of a suitable pharmacologically acceptable polymer, such as poly(ethyleneglycol) (PEG) or derivatives thereof (such as methoxypoly(ethyleneglycol) or mPEG). Generally, any suitable form of pegylation can be used, such as the pegylation used in the art for antibodies and antibody fragments (including but not limited to (single) domain antibodies and ScFvs); reference is made to, for example, Chapman, *Nat. Biotechnol.*, 54, 531-545 (2002); by Veronese and Harris, *Adv. Drug Deliv. Rev.* 54, 453-456 (2003), by Harris and Chess, *Nat. Rev. Drug. Discov.*, 2, (2003) and in WO04060965. Various reagents for pegylation of proteins are also commercially available, for example, from Nektar Therapeutics, USA. Preferably, site-directed pegylation is used, in particular via a cysteine-residue (see, for example, Yang et al., *Protein Engineering*, 16, 10, 761-770 (2003)). For example, for this purpose, PEG may be attached to a cysteine residue that naturally occurs in a nanobody of the invention, a nanobody of the invention may be modified so as to suitably

introduce one or more cysteine residues for attachment of PEG, or an amino acid sequence comprising one or more cysteine residues for attachment of PEG may be fused to the N- and/or C-terminus of a nanobody of the invention, all using techniques of protein engineering known per se to the skilled person. Preferably, for the immunoglobulin single variable domains and proteins of the invention, a PEG is used with a molecular weight of more than 5000, such as more than 10,000 and less than 200,000, such as less than 100,000; for example, in the range of 20,000-80,000. Another, usually less preferred modification comprises N-linked or O-linked glycosylation, usually as part of co-translational and/or post-translational modification, depending on the host cell used for expressing the immunoglobulin single variable domain or polypeptide of the invention. Another technique for increasing the half-life of an immunoglobulin single variable domain may comprise the engineering into bifunctional constructs (for example, one nanobody against the target MMR and one against a serum protein such as albumin) or into fusions of immunoglobulin single variable domains with peptides (for example, a peptide against a serum protein such as albumin).

Yet another modification may comprise the introduction of one or more detectable labels or other signal-generating groups or moieties, depending on the intended use of the labeled nanobody. Suitable labels and techniques for attaching, using and detecting them will be clear to the skilled person and, for example, include, but are not limited to, fluorescent labels (such as fluorescein, isothiocyanate, rhodamine, phycoerythrin, phycocyanin, allophycocyanin, o-phthaldehyde, and fluorescamine and fluorescent metals such as Eu or others metals from the lanthanide series), phosphorescent labels, chemiluminescent labels or bioluminescent labels (such as luminal, isoluminol, theromatic acridinium ester, imidazole, acridinium salts, oxalate ester, dioxetane or GFP and its analogs), radio-isotopes, metals, metals chelates or metallic cations or other metals or metallic cations that are particularly suited for use in vivo, in vitro or in situ diagnosis and imaging, as well as chromophores and enzymes (such as malate dehydrogenase, staphylococcal nuclease, delta-V-steroid isomerase, yeast alcohol dehydrogenase, alpha-glycerophosphate dehydrogenase, triose phosphate isomerase, biotinavidin peroxidase, horseradish peroxidase, alkaline phosphatase, asparaginase, glucose oxidase, beta-galactosidase, ribonuclease, urease, catalase, glucose-VI-phosphate dehydrogenase, glucoamylase and acetylcholine esterase). Other suitable labels will be clear to the skilled person and, for example, include moieties that can be detected using NMR or ESR spectroscopy. Such labeled nanobodies and polypeptides of the invention may, for example, be used for in vitro, in vivo or in situ assays (including immunoassays known per se such as ELISA, RIA, EIA and other "sandwich assays," etc.) as well as in vivo diagnostic and imaging purposes, depending on the choice of the specific label. As will be clear to the skilled person, another modification may involve the introduction of a chelating group, for example, to chelate one of the metals or metallic cations referred to above. Suitable chelating groups, for example, include, without limitation, diethyl-enetriamine-pentaacetic acid (DTPA) or ethylenediaminetetraacetic acid (EDTA). Yet another modification may comprise the introduction of a functional group that is one part of a specific binding pair, such as the biotin-(strept)avidin binding pair. Such a functional group may be used to link the nanobody of the invention to another protein, polypeptide or chemical compound that is bound to the other half of the binding pair, i.e., through formation of the binding pair. For example, a nanobody of the invention may be conjugated to biotin, and

linked to another protein, polypeptide, compound or carrier conjugated to avidin or streptavidin. For example, such a conjugated nanobody may be used as a reporter, for example, in a diagnostic system where a detectable signal-producing agent is conjugated to avidin or streptavidin. Such binding pairs may, for example, also be used to bind the nanobody of the invention to a carrier, including carriers suitable for pharmaceutical purposes. One non-limiting example are the liposomal formulations described by Cao and Suresh, *Journal of Drug Targeting*, 8, 4, 257 (2000). Such binding pairs may also be used to link a therapeutically active agent to the nanobody of the invention.

According to a preferred embodiment, the immunoglobulin single variable domain of the present invention is fused to a detectable label, either directly or through a linker. Preferably, the detectable label is a radio-isotope or radioactive tracer, which is suitable for medical applications, such as in vivo nuclear imaging. Examples include, without the purpose of being limitative, ^{99m}Tc , ^{123}I , ^{125}I , ^{111}In , ^{18}F , ^{64}Cu , ^{67}Ga , ^{68}Ga , and any other radio-isotope which can be used in animals, in particular mouse or human. According to a specific embodiment, the detectable label is ^{99m}Tc .

In still another embodiment, the immunoglobulin single variable domain of the present invention is fused to a moiety selected from the group consisting of a toxin, or to a cytotoxic drug, or to an enzyme capable of converting a prodrug into a cytotoxic drug, or to a radionuclide, or coupled to a cytotoxic cell, either directly or through a linker. Specific, but non-limiting examples of such moieties are described in the Example section.

As used herein, "linkers" are peptides of 1 to 50 amino acids length and are typically chosen or designed to be unstructured and flexible. These include, but are not limited to, synthetic peptides rich in Gly, Ser, Thr, Gln, Glu or further amino acids that are frequently associated with unstructured regions in natural proteins.⁽⁴⁹⁾ Non-limiting examples of suitable linker sequences are described in the Example section, and include (G₄S)₃ (GGGGSGGGSGGGGS; SEQ ID NO:121), llama IgG2 hinge (AHHSDDPSSKAPKAPMA; SEQ ID NO:122) or human IgA hinge (SPSTPTPSPSTP-PAS SEQ ID NO:123) linkers.

In a particular embodiment, the immunoglobulin single variable domains of the invention are in a "multivalent" form and are formed by bonding, chemically or by recombinant DNA techniques, together two or more monovalent immunoglobulin single variable domains. Non-limiting examples of multivalent constructs include "bivalent" constructs, "trivalent" constructs, "tetravalent" constructs, and so on. The immunoglobulin single variable domains comprised within a multivalent construct may be identical or different. In another particular embodiment, the immunoglobulin single variable domains of the invention are in a "multi-specific" form and are formed by bonding together two or more immunoglobulin single variable domains, of which at least one with a different specificity. Non-limiting examples of multi-specific constructs include "bi-specific" constructs, "tri-specific" constructs, "tetra-specific" constructs, and so on. To illustrate this further, any multivalent or multispecific (as defined herein) immunoglobulin single variable domain of the invention may be suitably directed against two or more different epitopes on the same antigen, for example, against two or more different parts of the MMR ectodomain; or may be directed against two or more different antigens, for example, against MMR and one or more other marker of Table 1. Preferably, a monovalent immunoglobulin single variable domain of the invention is such that it will bind to the MMR (as described herein) with an affinity less than 500 nM, preferably less than 200 nM,

more preferably less than 10 nM, such as less than 500 μ M. Multivalent or multispecific immunoglobulin single variable domains of the invention may also have (or be engineered and/or selected for) increased avidity and/or improved selectivity for the desired MMR, and/or for any other desired property or combination of desired properties that may be obtained by the use of such multivalent or multispecific immunoglobulin single variable domains.

In a further aspect, the present invention also provides a polypeptide comprising any of the immunoglobulin single variable domains according to the invention, either in a monovalent, multivalent or multi-specific form. Thus, polypeptides comprising monovalent, multivalent or multi-specific nanobodies are included here as non-limiting examples.

In still another aspect, the invention also relates to a pharmaceutical composition comprising a therapeutically effective amount of an immunoglobulin single variable domain of the invention, and at least one of pharmaceutically acceptable carrier, adjuvant or diluent.

A "carrier," or "adjuvant," in particular a "pharmaceutically acceptable carrier" or "pharmaceutically acceptable adjuvant" is any suitable excipient, diluent, carrier and/or adjuvant which, by themselves, do not induce the production of antibodies harmful to the individual receiving the composition nor do they elicit protection. So, pharmaceutically acceptable carriers are inherently non-toxic and nontherapeutic, and they are known to the person skilled in the art. Suitable carriers or adjuvantia typically comprise one or more of the compounds included in the following non-exhaustive list: large slowly metabolized macromolecules such as proteins, polysaccharides, polylactic acids, polyglycolic acids, polymeric amino acids, amino acid copolymers and inactive virus particles. Carriers or adjuvants may be, as a non limiting example, Ringer's solution, dextrose solution or Hank's solution. Non aqueous solutions such as fixed oils and ethyl oleate may also be used. A preferred excipient is 5% dextrose in saline. The excipient may contain minor amounts of additives such as substances that enhance isotonicity and chemical stability, including buffers and preservatives.

As used herein, the terms "therapeutically effective amount," "therapeutically effective dose" and "effective amount" mean the amount needed to achieve the desired result or results. As used herein, "pharmaceutically acceptable" means a material that is not biologically or otherwise undesirable, i.e., the material may be administered to an individual along with the compound without causing any undesirable biological effects or interacting in a deleterious manner with any of the other components of the pharmaceutical composition in which it is contained.

Certain of the above-described immunoglobulin single variable domains may have therapeutic utility and may be administered to a subject having a condition in order to treat the subject for the condition.

Accordingly, in a second aspect, the invention relates to a method of preventing and/or treating cancer, comprising administering a pharmaceutically effective amount of an immunoglobulin single variable domain of the invention or a pharmaceutical composition derived thereof to a subject in need thereof.

As used herein, the term "preventing cancer" means inhibiting or reversing the onset of the disease, inhibiting or reversing the initial signs of the disease, inhibiting the appearance of clinical symptoms of the disease. As used herein, "treating cancer" or "treating a subject or individual having cancer" includes substantially inhibiting the disease, substantially slowing or reversing the progression of the disease, substan-

tially ameliorating clinical symptoms of the disease or substantially preventing the appearance of clinical symptoms of the disease. In particular, it includes inhibition of the replication of cancer cells, inhibition of the spread of cancer, reduction in tumor size, lessening or reducing the number of cancerous cells in the body, and/or amelioration or alleviation of the symptoms of cancer. A treatment is considered therapeutic if there is a decrease in mortality and/or morbidity, and may be performed prophylactically, or therapeutically. A variety of subjects or individuals are treatable. Generally the "subjects" are mammals or mammalian, where these terms are used broadly to describe organisms which are within the class mammalia, including the orders carnivore (e.g., dogs and cats), rodentia (e.g., mice, guinea pigs, and rats), and primates (e.g., humans, chimpanzees, and monkeys). In many embodiments, the subjects will be humans.

As used herein, the term "cancer" refers to any neoplastic disorder, including such cellular disorders as, for example, renal cell cancer, Kaposi's sarcoma, chronic leukemia, breast cancer, sarcoma, ovarian carcinoma, rectal cancer, throat cancer, melanoma, colon cancer, bladder cancer, mastocytoma, lung cancer, mammary adenocarcinoma, pharyngeal squamous cell carcinoma, and gastrointestinal or stomach cancer.

In a specific embodiment, the invention relates to a method of inhibiting tumor growth or tumor metastases in a mammal in need thereof comprising selectively targeting TAM subpopulations linked to different intratumoral regions, such as hypoxic or normoxic regions of a solid tumor. As a specific embodiment, the above method comprises administering to the mammal a pharmaceutically effective amount of an immunoglobulin single variable domain or a pharmaceutical composition or a polypeptide according to the invention, in particular an immunoglobulin single variable domain fused to a toxin, or to a cytotoxic drug, or to an enzyme capable of converting a prodrug into a cytotoxic drug, or to a radionuclide, or coupled to a cytotoxic cell, and the like (see also Example section).

As used herein, "TAM subpopulations" refer to distinct subsets of tumor-associated macrophages (TAMs) that are present in a tumor environment, which are characterized by the differential expression of molecular markers. For a detailed description of different TAM subpopulations, reference is made to the Example section, in particular Examples 1 to 8, and Example 24, and Table 1. For example, the macrophage mannose receptor is one of the molecular markers which is specifically expressed on a TAM subpopulation which resides predominantly in the hypoxic regions of a tumor. According to particular embodiments, a TAM subpopulation can be defined as MHC II^{low} or MHC II^{hi}. In a preferred embodiment, the TAM subpopulation is defined as MHC II^{low}.

The immunoglobulin single variable domain and/or pharmaceutical composition may be administered by any suitable method within the knowledge of the skilled man. The administration of a nanobody as described above or a pharmaceutically acceptable salt thereof may be by way of oral, inhaled or parenteral administration. In particular embodiments the nanobody is delivered through intrathecal or intracerebroventricular administration. The active compound may be administered alone or preferably formulated as a pharmaceutical composition. An amount effective to treat a certain disease or disorder that express the antigen recognized by the nanobody depends on the usual factors such as the nature and severity of the disorder being treated and the weight of the mammal. However, a unit dose will normally be in the range of 0.01 to 50 mg, for example, 0.01 to 10 mg, or 0.05 to 2 mg of nanobody or a pharmaceutically acceptable salt thereof. Unit

doses will normally be administered once or more than once a day, for example, two, three, or four times a day, more usually one to three times a day, such that the total daily dose is normally in the range of 0.0001 to 1 mg/kg; thus a suitable total daily dose for a 70 kg adult is 0.01 to 50 mg, for example, 0.01 to 10 mg or more usually 0.05 to 10 mg. It is greatly preferred that the compound or a pharmaceutically acceptable salt thereof is administered in the form of a unit-dose composition, such as a unit dose oral, parenteral, or inhaled composition. Such compositions are prepared by admixture and are suitably adapted for oral, inhaled or parenteral administration, and as such may be in the form of tablets, capsules, oral liquid preparations, powders, granules, lozenges, reconstitutable powders, injectable and infusible solutions or suspensions or suppositories or aerosols. Tablets and capsules for oral administration are usually presented in a unit dose, and contain conventional excipients such as binding agents, fillers, diluents, tableting agents, lubricants, disintegrants, colorants, flavorings, and wetting agents. The tablets may be coated according to well known methods in the art. Suitable fillers for use include cellulose, mannitol, lactose and other similar agents. Suitable disintegrants include starch, polyvinylpyrrolidone and starch derivatives such as sodium starch glycolate. Suitable lubricants include, for example, magnesium stearate. Suitable pharmaceutically acceptable wetting agents include sodium lauryl sulphate. These solid oral compositions may be prepared by conventional methods of blending, filling, tableting or the like. Repeated blending operations may be used to distribute the active agent throughout those compositions employing large quantities of fillers. Such operations are, of course, conventional in the art. Oral liquid preparations may be in the form of, for example, aqueous or oily suspensions, solutions, emulsions, syrups, or elixirs, or may be presented as a dry product for reconstitution with water or other suitable vehicle before use. Such liquid preparations may contain conventional additives such as suspending agents, for example, sorbitol, syrup, methyl cellulose, gelatin, hydroxyethylcellulose, carboxymethyl cellulose, aluminium stearate gel or hydrogenated edible fats, emulsifying agents, for example, lecithin, sorbitan monooleate, or acacia; non-aqueous vehicles (which may include edible oils), for example, almond oil, fractionated coconut oil, oily esters such as esters of glycerine, propylene glycol, or ethyl alcohol; preservatives, for example, methyl or propyl p-hydroxybenzoate or sorbic acid, and if desired conventional flavoring or coloring agents. Oral formulations also include conventional sustained release formulations, such as tablets or granules having an enteric coating. Preferably, compositions for inhalation are presented for administration to the respiratory tract as a snuff or an aerosol or solution for a nebulizer, or as a microfine powder for insufflation, alone or in combination with an inert carrier such as lactose. In such a case the particles of active compound suitably have diameters of less than 50 microns, preferably less than 10 microns, for example, between 1 and 5 microns, such as between 2 and 5 microns. A favored inhaled dose will be in the range of 0.05 to 2 mg, for example, 0.05 to 0.5 mg, 0.1 to 1 mg or 0.5 to 2 mg. For parenteral administration, fluid unit dose forms are prepared containing a compound of the present invention and a sterile vehicle. The active compound, depending on the vehicle and the concentration, can be either suspended or dissolved. Parenteral solutions are normally prepared by dissolving the compound in a vehicle and filter sterilizing before filling into a suitable vial or ampoule and sealing. Advantageously, adjuvants such as a local anesthetic, preservatives and buffering agents are also dissolved in the vehicle. To enhance the stability, the composition can be frozen after

filling into the vial and the water removed under vacuum. Parenteral suspensions are prepared in substantially the same manner except that the compound is suspended in the vehicle instead of being dissolved and sterilized by exposure to ethylene oxide before suspending in the sterile vehicle. Advantageously, a surfactant or wetting agent is included in the composition to facilitate uniform distribution of the active compound. Where appropriate, small amounts of bronchodilators, for example, sympathomimetic amines such as isoprenaline, isoetharine, salbutamol, phenylephrine and ephedrine; xanthine derivatives such as theophylline and aminophylline and corticosteroids such as prednisolone and adrenal stimulants such as ACTH may be included. As is common practice, the compositions will usually be accompanied by written or printed directions for use in the medical treatment concerned. All these medicaments can be intended for human or veterinary use.

The efficacy of the immunoglobulin single variable domains of the invention, and of compositions comprising the same, can be tested using any suitable *in vitro* assay, cell-based assay, *in vivo* assay and/or animal model known *per se*, or any combination thereof, depending on the specific disease or disorder involved.

In a specific embodiment it should be clear that the therapeutic method of the present invention against cancer can also be used in combination with any other cancer therapy known in the art such as irradiation, chemotherapy or surgery.

Reliable hypoxia tracers that can be used for non-invasive tumor imaging are currently unavailable or limiting. The availability of such tracers would represent a significant progress in the field of radiotherapy, since they would allow the radiotherapist to adapt the radiation dose, depending on the targeted tumor region (hypoxic versus normoxic). The identification of tumor-associated macrophage (TAM) subsets that are situated in hypoxic/normoxic environments allows for the identification of macrophage-specific biomarkers that can be used for non-invasive imaging of hypoxic/normoxic areas in tumors. For example, MMR represents such a marker, since it is preferentially expressed on the hypoxic MHC II^{low} TAMs. Due to their small size and high tumor penetrance, nanobodies are the ideal format for non-invasive imaging. Nanobodies raised against markers that are preferentially expressed on the hypoxic MHC II^{low} TAMs can be used for the imaging of hypoxia in tumors. The anti-MMR nanobodies can be used in this respect.

Other applications of TAM subset-specific nanobodies, coupled to tracers for imaging (for example, Near Infrared Fluorescent or NIRF tracers), include but are not limited to (i) accurately quantifying the amount of TAM or TAM subsets inside any given tumor, which can be of prognostic value, (ii) assessing the impact of therapy—including TAM-directed therapies as presently claimed—on the amount and/or the activation state of TAM, (iii) visualizing hypoxic/normoxic regions within the tumor.

Accordingly, in a further aspect, the present invention also encompasses a method of *in vivo* imaging tumor cells in a subject, the method comprising the step of:

administering to the subject an immunoglobulin single variable domain according to the invention fused to a detectable label.

As used herein, “tumor cells” or simply “tumor” refers to the tumor tissue as a whole, including different cell types that are present in a tumor environment. Tumor cells include cancer cells but also non-transformed host cells, or tumor-associated stroma cells. Examples of tumor-associated stroma cells include myeloid cells, in particular tumor-associated macrophages.

Preferably, the above described method may further comprise one or more of the following steps of:

selectively targeting and/or visualizing tumor-associated macrophage (TAM) subpopulations linked to different intratumoral regions, in particular wherein the intratumoral regions include a hypoxic or normoxic region of a solid tumor;

determining a relative percentage of the TAM subpopulations, and optionally assessing the impact of a cancer therapy on the relative percentage of the tumor-associated macrophage subpopulations;

Further, in still another aspect, the present invention envisages a method of diagnosing cancer or prognosing cancer aggressiveness in a subject suffering from or suspected to suffer from cancer comprising the steps of:

utilizing any of the immunoglobulin single variable domains according to the invention to determine the relative percentage of tumor-associated macrophage subpopulations in the subject; and

diagnosing cancer or prognosing cancer aggressiveness in the subject according to the relative percentage of the TAM subpopulations; and optionally

assessing the impact of a cancer therapy on the relative percentage of the tumor-associated macrophage subpopulations.

In particular embodiments, the method comprises the steps of (i) providing a sample from the individual comprising cancer cells or suspected to comprise cancer cells; (ii) determining in the sample the relative percentage of TAM subpopulations; (iii) classifying the individual as having a good/prognosis or diagnosing the individual as having cancer according to the results of step (ii). To further illustrate this, reference is made to Example 19.

A sample may comprise any clinically relevant tissue sample, such as a tumor biopsy or fine needle aspirate, or a sample of bodily fluid, such as blood, plasma, serum, lymph, ascitic fluid, cystic fluid, urine or nipple exudate. The sample may be taken from a human, or, in a veterinary context, from non-human animals such as ruminants, horses, swine or sheep, or from domestic companion animals such as felines and canines. The sample may also be paraffin-embedded tissue sections. It is understood that the cancer tissue includes the primary tumor tissue as well as a organ-specific or tissue-specific metastasis tissue.

In the context of the present invention, prognosing an individual suffering from or suspected to suffer from cancer refers to a prediction of the survival probability of individual having cancer or relapse risk which is related to the invasive or metastatic behavior (i.e., malignant progression) of tumor tissue or cells. As used herein, "good prognosis" means a desired outcome. For example, in the context of cancer, a good prognosis may be an expectation of no recurrences or metastasis within two, three, four, five years or more of initial diagnosis of cancer. "Poor prognosis" means an undesired outcome. For example, in the context of cancer, a poor prognosis may be an expectation of a recurrence or metastasis within two, three, four, or five years of initial diagnosis of cancer. Poor prognosis of cancer may indicate that a tumor is relatively aggressive, while good prognosis may indicate that a tumor is relatively nonaggressive.

As used herein, the terms "determining," "measuring," "assessing," and "assaying" are used interchangeably and include both quantitative and qualitative determinations. In particular, ways to determine the relative percentage of TAM subpopulations are known to the person skilled in the art, for

example, by using flow cytometry, and is illustrated into more detail, but without the purpose of being limitative, in the Example section.

Next, it is commonly known that finding tumor-specific markers for antibody-based targeting remains a difficult task. This is especially true when targeting the tumor stroma, since stromal antigens are typically not restricted to tumors. This may hamper the usefulness of these tools both for diagnostic and therapeutic applications. Therefore, a strategy was developed to reduce the targeting of tracers to healthy organs to background levels, while preserving an efficient targeting of the tumor. Unexpectedly, it was found that co-injecting monovalent labeled nanobody directed against the macrophage mannose receptor and excess of unlabeled bivalent immunoglobulin single variable domain directed against the same target, blocked all extratumoral sites, while only slightly affecting tumor-specific tracer uptake. The monovalent-labeled—bivalent-unlabeled immunoglobulin single variable domain approach as described herein is especially attractive since bivalent immunoglobulin single variable domains do not efficiently compete for free binding sites in the tumor, while they block extratumoral sites much more efficiently.

Thus, according to a preferred embodiment, any of the above described methods for in vivo imaging, diagnosis/prognosis or treatment of cancer may comprise an additional step of co-administering a monovalent labeled immunoglobulin single variable domain according to the invention and an unlabeled bivalent form of an immunoglobulin single variable domain directed against the same target (macrophage mannose receptor) to block extratumoral binding sites. According to a preferred embodiment, the unlabeled bivalent form of the anti-MMR immunoglobulin single variable domain may comprise two identical or two different immunoglobulin single variable domains, as long as at least one of the immunoglobulin single variable domains is directed against the same target (macrophage mannose receptor). As used herein, "unlabeled" refers to the absence of a detectable label, in particular a radio-isotope or radio-active tracer as defined hereinbefore. It should be clear that this does not exclude the absence of another modification (as defined hereinbefore).

A further aspect of the invention relates to a method for producing an immunoglobulin single variable domain according to the invention or a polypeptide comprising an immunoglobulin single variable domain according to the invention, the method comprising the steps of:

expressing, in a suitable host cell or expression system, a nucleic acid sequence encoding an immunoglobulin single variable domain or a polypeptide comprising an immunoglobulin single variable domain according to the invention; and optionally isolating and/or purifying the immunoglobulin single variable domain or the polypeptide.

Suitable expression systems include constitutive and inducible expression systems in bacteria or yeasts, virus expression systems, such as baculovirus, semliki forest virus and lentiviruses, or transient transfection in insect or mammalian cells. Suitable host cells include *E. coli*, *Lactococcus lactis*, *Saccharomyces cerevisiae*, *Schizosaccharomyces pombe*, *Pichia pastoris*, and the like. Suitable animal host cells include HEK 293, COS, S2, CHO, NSO, DT40 and the like. The cloning, expression and/or purification of the immunoglobulin single variable domains can be done according to techniques known by the skilled person in the art.

The following examples more fully illustrate preferred features of the invention, but are not intended to limit the inven-

tion in any way. Those having ordinary skill in the art and access to the teachings herein will recognize additional modifications and embodiments within the scope thereof. Therefore, the present invention is limited only by the claims attached herein. All of the starting materials and reagents disclosed below are known to those skilled in the art, and are available commercially or can be prepared using well-known techniques.

EXAMPLES

Material and Methods to the Examples

Mice and Cell Lines

Female Balb/c and C57BL/6 mice were purchased from Harlan. Balb/c CX₃CR1^{GFP/GFP} mice were a gift from Dr. Grégoire Lauvau (Universite de Nice-Sophia Antipolis, France) and Dr. Frédéric Geissmann (King's College London, UK). C57BL/6 MMR-deficient, CCR2-deficient and MMTVPyMT mice were provided by Etienne Pays (Universite Libre de Bruxelles), Frank Tacke (Aachen University) and Massimiliano Mazzone (KULeuven), respectively. All animal studies were approved by and performed according to the guidelines of the institutional review board. The Balb/c mammary adenocarcinoma cell line) TS/A⁽¹⁰⁾ was provided by Dr. Vincenzo Bronte (Istituto Oncologico Veneto, Italy). The Balb/c mammary adenocarcinoma TS/A and 3LL-R clone of the C57BL/6 Lewis Lung Carcinoma and were injected subcutaneously (sc) in the flank or in the fat pads (3×10⁶ cells). 12 to 14 days after inoculation, TS/A and 3LL-R tumor-bearing mice were imaged. MMTV-PyMT mice bearing macroscopic tumors were consecutively imaged with distinct tracers 48 to 72 hours apart. Tumor dissection and flow cytometry were performed 96 hours after the last scan.

Tumor Preparation, Flow Cytometry and Cell Sorting

Tumors were chopped and incubated for 25 minutes (37° C.) with 10 U/ml Collagenase typel, 400 U/ml Collagenase typeIV and 30 U/ml DNaseI (Worthington). Density gradients (Axis-Shield) were used to remove tissue debris and dead cells.

Commercial antibodies used for cell surface stainings are found in Table 2. Non-labeled anti-CCR2 (MC-21) was a gift of Dr. Matthias Mack (University of Regensburg, Germany). To prevent aspecific binding, rat anti-mouse CD16/CD32 (clone 2.4G2, BD Biosciences) was used. Nanobodies were labeled using Nanobodies[®] 488 or Alexafluor[®] 647 Protein Labeling kit (Invitrogen) according to the manufacturers' instructions.

To purify TAMs, CD11b⁺ cells were isolated via MACS using anti-CD11b microbeads (Miltenyi Biotec). Subsequently, cells were sorted using a BD FACSARIA[™] II (BD Biosciences).

In Vivo Labeling of Blood Monocytes

Latex labeling of blood monocytes was performed as described earlier.^(19,20) Briefly, to label Ly6C^{low} monocytes and track their infiltration in tumors, mice were injected intravenously (iv) with 250 µl of 0.5 µm fluoresbrite yellow-green microspheres (Polysciences) diluted 1:25 in PBS. Twenty-four hours later, mice received sc TS/A injections. To label and track Ly6C^{hi} monocytes, mice were injected iv with 250 µl of clodronate liposomes. Eighteen hours later, mice received iv latex injection and sc TS/A injection. Clodronate was a gift from Roche and was incorporated into liposomes as previously described.⁽²¹⁾

Bromodeoxyuridine Labeling and Ki67 Stainings

Tumor-bearing mice (14 days pi) were given an initial intraperitoneal injection of 1 mg BrdU (BD Biosciences),

followed by continuous BrdU administration in the drinking water at a concentration of 0.8 mg/ml (Sigma). Tumors were collected after consecutive time points and BrdU intracellular stainings were performed following the manufacturer's instructions (BrdU labeling Kit, BD Biosciences). PE-labeled anti-Ki67 or matching isotype controls (BD Biosciences) was added together with FITC-labeled anti-BrdU in the final step of the intracellular staining protocol.

RNA Extraction, cDNA Preparation and Quantitative Real-Time PCR

RNA was extracted using TRIzol (Invitrogen) and was reverse-transcribed with oligo(dT) and SuperScript II RT (Invitrogen), following the manufacturer's instructions. Quantitative real-time PCR was performed in an iCycler, with iQ SYBR Green Supermix (Bio-Rad) using gene-specific primers (Table 2). PCR cycles consisted of 1-minute denaturation at 94° C., 45-second annealing at 55° C., and 1-minute extension at 72° C. Gene expression was normalized according to the expression of ribosomal protein S12.

Intracellular TNFα and iNOS Stainings

For intracellular TNFα stainings, freshly isolated TAMs were cultured in vitro for 1 hour, after which Brefeldin A (BD Biosciences) was added. Five hours later cells were fixed, permeabilized (Fix/Perm kit, eBioscience) and stained with anti-TNFα. For intracellular iNOS stainings, freshly isolated TAMs were cultured in vitro with or without 10 U/ml IFNγ and/or 10 ng/ml LPS. 12 hours later cells were fixed, permeabilized and stained with anti-iNOS. Normalized delta-Median Fluorescence Intensity (AMFI) was calculated as follows: [(MFI iNOS staining)–(MFI isotype staining)]/(MFI iNOS staining) FACS data were acquired using a BD FACS-Canto II (BD Biosciences).

Measurement of Arginase Activity

The arginase activity in the lysate of 5 10⁵ sorted TAMs was measured as described earlier.⁽²²⁾

Immunohistochemistry and Hypoxia Measurements

For hypoxia stainings, tumor-bearing mice were injected with 80 mg/kg body weight pimonidazole (Hypoxyprobe-1, HP-1, HPI Inc.) and 2 hours later tumors were collected.

For immunohistochemistry, tumors were snap-frozen in liquid nitrogen and 5 µm sections were made. Sections were fixed for 10 minutes in ice-cold acetone. To block aspecific binding sites, sections were incubated 30 minutes with 10% normal donkey serum (Jackson ImmunoResearch Laboratories). For CD11b, MHC II and anti-HP-1 triple stainings, sections were: (1) incubated 30 minutes with purified rat anti-CD11b (BD Biosciences) and purified rabbit anti-HP-1 (HPI Inc.) (2) incubated 30 minutes with F(ab')₂ donkey anti-Rat/Cy3 (Jackson ImmunoResearch Laboratories) and F(ab')₂ donkey anti-rabbit/Cy5 (Jackson ImmunoResearch Laboratories) (3) remaining anti-rat binding sites were blocked with 5% normal rat serum (Jackson ImmunoResearch Laboratories) (4) incubated 30 minutes with rat anti-MHC II/alexa-fluor 488 (M5/114.15.2 Biolegend). Rat anti-MECA32 (Pan-endothelial cell antigen) was from BD Biosciences. Sections were mounted with fluorescent mounting medium (Dako). Pictures were acquired with a Plan-Neofluar 10×/0.30 or Plan-Neofluar 20×/0.50 (Carl Zeiss) objective on a Zeiss Axioplan 2 microscope (Carl Zeiss) equipped with an Orca-R2 camera (Hamamatsu) and Smartcapture 3 software (Digital Scientific UK). For flow cytometric HP-1 measurements, tumor single cell suspensions were made, and cells were fixed and permeabilized using the BD Biosciences Fix/Perm kit. Finally, rat anti-HP1/FITC (HPI Inc.) was added for 30 minutes at 37° C.

Determining Latex Phagocytosis In Vivo and In Vitro

For measuring in vivo latex uptake by TAMs, tumor-bearing mice were injected iv with 250 μ l of yellow-green latex microspheres (Polysciences) diluted 1:25 in PBS. 1-2 hours later, tumor single cell suspensions were made and latex uptake by tumor CD11b⁺ cells was assessed via FACS. For in vitro latex uptake, freshly isolated TAMs were cultured in 96-well plates for 40 minutes at 4° C. or 37° C., in the presence of latex (diluted 1:5000).

Chorioallantoic Membrane Angiogenesis Assays

Chorioallantoic membrane (CAM) assays were performed as described earlier.⁽²³⁾ Briefly, fertilized white leghorn chicken eggs (Wyverkens, Halle, Belgium) were incubated at 37° C. for three days prior to removing 3 ml of albumen to detach the shell from the developing CAM. Next, a window was made in the eggshell to expose the CAM. At day 9, sterile absorbable gelatin sponges (1-2 mm³; Hospithera, Brussels, Belgium) were impregnated with 5×10⁴ sorted TAM subsets and placed on the CAM. Sponges were also loaded with PBS/0.1% BSA (1 mg/ml, <50 μ g/embryo) as negative control and with recombinant human VEGF-A₁₆₅ (100 μ g/ml, <5 μ g/embryo) as positive control. At day 13, membranes were fixed with 4% paraformaldehyde and the area around the implants was analyzed using a Zeiss Lumar V.12 stereomicroscope with NeoLumar S1.5× objective (15× magnification). Digital images were captured using an AxioCam MRC5 and processed with Axiovision 4.5 Software (Zeiss). To determine the number of blood vessels, a grid containing three concentric circles with diameters of 4, 5, and 6 mm was positioned on the surface of the CAM and all vessels radiating from the sample spot and intersecting the circles were counted under a stereomicroscope.

DQ-OVA Processing, MLR Assays, Suppression Assays

To assess TAM antigen processing, tumor single cell suspensions were incubated for 15 minutes at 0° C. or 37° C. in the presence of 10 μ g/ml DQ-OVA (Molecular Probes), allowing for antigen uptake. After thorough washing, cells could further process DQ-OVA intracellularly during different time intervals, at 0° C. or 37° C. Following each time interval, cells were surface labeled and DQ-OVA fluorescence in each TAM subset was measured via FACS.

For Mixed Leukocyte Reaction (MLR) assays, T cells were purified from C57BL/6 spleens, by first depleting CD11c⁺ and CD19⁺ cells on a MACS LD column using anti-CD11c and anti-CD19 microbeads (Miltenyi biotech) and subsequently positively selecting CD4⁺ or CD8⁺ T cells using anti-CD4 or anti-CD8 microbeads (Miltenyi biotech). 2×10⁵ purified C57BL/6 T cells were cultured with 5×10⁴ sorted Balb/c TAMs or cDCs, in round-bottom 96-well plates. Three days later ³H-thymidine was added and cells were allowed to proliferate for another 18 hours before incorporated radioactivity was measured.

For T-cell suppression assays, 1×10⁵ (1:2), 5×10⁴ (1:4), 2.5×10⁴ (1:8) or 1.25×10⁴ (1:16) sorted TAMs or cDCs were added to 2×10⁵ naive Balb/c splenocytes, in flat-bottom 96-well plates. These co-cultures were promptly stimulated with 1 μ g/ml anti-CD3, 24 hours later ³H-thymidine was added and cells were allowed to proliferate for another 18 hours before incorporated radioactivity was measured. L-NMMA (0.5 mM, Sigma), nor-NOHA (0.5 mM, Calbiochem), or both, were added from the beginning of the culture. The Relative % suppression of proliferation was calculated as described earlier:⁽²⁴⁾ (% Suppression without inhibitor)/(% Suppression with inhibitor)×100, with % Suppression calculated as [1-(proliferation of splenocytes)/(proliferation splenocytes+TAMs)]×100.

Sorting of Splenic Conventional DCs

To purify splenic conventional DCs, spleens were flushed with 200 U/ml collagenase III (Worthington) and squashed. Subsequently, CD11c⁺ cells were enriched via MACS, using anti-CD11c microbeads (Miltenyi Biotec), after which CD11c⁺MHC II^{hi}B220⁺Ly6C⁺ DCs were sorted using a BD FACSARIA™ II (BD Biosciences).

Statistics

Statistical significance was determined by the Student's t test, using Microsoft Excel or GraphPad Prism 4.0 software. Differences were considered significant when P≤0.05. Geometric means and confidence intervals were determined using Microsoft Excel.

Where multiple comparisons are made (nine to ten different organs), the p-values of the student's t test were adjusted by Holm's procedure.⁽⁴²⁾ The R environment⁽⁴³⁾ and the multtest package⁽⁴⁴⁾ were used for statistical analyses and figures. The significance of the student t tests and corrections for multiple testing was set to 0.05.

Generation of Mono- and Bivalent Anti-MMR Nanobodies

The anti-MMR Nanobody (Nb) clone 1 was isolated from an immune phage library in a similar way as described before.^(30,31) In brief, an alpaca (Vicugna pacos) was immunized with 100 μ g MMR (R&D Systems) six times at weekly intervals. mRNA prepared from peripheral blood lymphocytes was used to make cDNA with the Ready-to-Go You-prime-first-strand beads (GE Healthcare). The gene sequences encoding the VHHs were PCR amplified using the CALL001/CALL002 and A6E/38 primer pairs. These PCR fragments were ligated into the pHEN4 phagemid vector after digestion with the PstI and BstEII restriction enzymes. Using M13K07 helper phage infection, the VHH library was expressed on phages and specific Nanobody-phages were enriched by several consecutive rounds of in vitro selection on microtiter plates (Nunc). Individual colonies were screened in ELISA for antigen recognition with non-specific phage particles serving as a negative control. The VHH genes of the clones that scored positive in ELISA were recloned into the expression vector pHEN6 using the restriction enzymes PstI and BstEII. Expression in the periplasm and purification of Nanobody was performed as described previously.⁽²⁸⁾

Bivalent Nanobodies were generated by recombinantly attaching a linker sequence 3' of the VHH sequence using PCR primer biNbF (5'-CCG GCC ATG GCC CAG GTG CAG CTT CAG GAG TCT GG AGG AGG-3'; SEQ ID NO:117) and primers biNbG4SR (5'-TGA TTC CTG CAG CTG CAC CTG ACT ACC GCC GCC TCC AGA TCC ACC TCC GCC ACT ACC GCC TCC GCC TGA GGA GAC GGT GAC CTG GGT C-3'; SEQ ID NO:118), biNbG2cR (5'-TGA TTC CTG CAG CTG CAC CTG TGC CAT TGG AGC TTT GGG AGC TTT GGA GCT GGG GTC TTC GCT GTG GTG CGC TGA GGA GAC GGT GAC CTG GGT C-3'; SEQ ID NO:119), biNbIgAR (5'-TGA TTC CTG CAG CTG CAC CTG ACT TGC CGG TGG TGT GGA TGG TGA TGG TGT GGG AGG TGT AGA TGG GCT TGA GGA GAC GGT GAC CTG GGT C-3'; SEQ ID NO:120) which code for a (G₄S)₃ (GGGGSGGGSGGGGS; SEQ ID NO:121), llama IgG2 hinge (AHHSEDPSSKAPKAPMA; SEQ ID NO:122) or human IgA hinge (SPSTPPTPSPSTPPAS; SEQ ID NO:123) linker respectively. These PCR fragments were inserted 5' of the VHH gene in the original VHH expression vector with a PstI/BstEII restriction digest. After ligation, the resulting bivalent anti-MMR Nanobody vector was expressed as described above.

Construction and Production Anti-MMR-PE38 Immunotoxins

Anti-MMR-PE38 toxin fusions were generated using the anti-MMR bivalent Nanobodies as templates. The PE38 (re-

combinant *Pseudomonas* Exotoxin A⁽³³⁾ gene was PCR amplified from the pET28aCD11scFv-PE38 vector⁽³²⁾ using the PE38HF (5'-ATT GAA TTC TAT TAG TGG TGG TGG TGG TGG TGC TCG AGT G -3'; SEQ ID NO:124) and PE38bisR (5'-TTA ACT GCA GAT GGC CGA AGA GGG CGG CAG CCT-3'; SEQ ID NO:125) primers. During this PCR reaction a PstI and EcoRI restriction site were introduced 5' and 3' of the PE38 gene respectively. Both the PE38 PCR fragments and the pHEN6 vectors containing bivalent anti-MMR Nanobody genes with a (G₄S)₃ (GGGGSGGGSGGGGS; SEQ ID NO:121), llama IgG2 hinge (AHHSEDPSSKAPKAPMA; SEQ ID NO:122) or human IgA hinge (SPSTPPTSPSTPPAS; SEQ ID NO:123) linker were digested using PstI and EcoRI restriction enzymes. By ligating the PE38 gene fragment in the pHEN6 vector fragments, the PE38 gene was fused to the 3' end of the anti-MMR Nanobody-linker gene. The resulting immunotoxin constructs were produced and purified in the same manner as the mono- and bivalent anti-MMR Nanobody constructs.

Surface Plasmon Resonance

Affinity analysis was performed using a BIAcore T100 (GE Healthcare) with HEPES-buffered saline running buffer (10 mM HEPES with 0.15 M NaCl, 3.4 mM EDTA and 0.005% surfactant P20 at pH 7.4). MRR was immobilized on a CM5 chip in acetate buffer 50 mM (pH 5.0), resulting in 2100 RU MMR coated on the chip. A second channel on the same chip was activated/deactivated in a similar way and served as a negative control. The MMR Nanobodies were used as analytes in eleven different concentrations, ranging from 1 to 2000 nM, at a flow rate of 10 ml/min. Glycine-HCl 50 mM (pH 2.0) was used for elution. The kinetic and equilibrium parameters (k_d, k_a and K_D) values were calculated from the combined sensogram of all concentrations using BIAcore T100 evaluation software 2.02 (GE Healthcare).

Nanobody Purification

All Nanobody proteins were purified from *E. coli* periplasmic extracts using immobilized metal affinity chromatography (IMAC) on Ni-NTA resin (Sigma-Aldrich, St. Louis, Mo.) followed by size exclusion chromatography (SEC) on Superdex 75 HR 10/30 (Pharmacia, Gaithersburg, Md.) in phosphate buffered saline pH 7.4 (PBS).

Nanobody Labeling and In Vitro Characterization of ^{99m}Tc-Labeled Nanobodies

Nanobodies were labeled with ^{99m}Tc at their hexahistidine tail. For the labeling, [^{99m}Tc(H₂O)₃(CO)₃]⁺ was synthesized by adding 1 mL of ^{99m}TcO₄⁻ (0.74-3.7 GBq) to an Isolink kit (Mallinckrodt Medical BV) containing 4.5 mg of sodium boranocarbonate, 2.85 mg of sodium tetraborate.10H₂O, 8.5 mg of sodium tartrate.2H₂O, and 7.15 mg of sodium carbonate, pH 10.5. The vial was incubated at 100° C. in a boiling bath for 20 minutes. The freshly prepared [^{99m}Tc(H₂O)₃(CO)₃]⁺ was allowed to cool at room temperature for 5 minutes and neutralized with 125 µL of 1 M HCl to pH 7-8. [^{99m}Tc(H₂O)₃(CO)₃]⁺ was added to 50 µL of 1 mg/mL monovalent Nanobody or 2 mg/mL bivalent Nanobody, together with 50 µL of carbonate buffer, pH 8. The mixture was incubated for 90 minutes at 52° C. in a water bath. The labeling efficiency was determined by instant thin-layer chromatography in acetone as mobile phase and analyzed using a radiometric chromatogram scanner (VCS-201; Veenstra). When the labeling yield was less than 90%, the ^{99m}Tc-Nanobody solution was purified on a NAP-5 column (GE Healthcare) pre-equilibrated with phosphate-buffered saline (PBS) and passed through a 0.22 µm Millipore filter to eliminate possible aggregates.

Pinhole SPECT-microCT Imaging Procedure

Mice were intravenously injected with 100-200 µl 45-155 MBq (about 5-10 µg) of ^{99m}Tc-Nanobody, with or without an excess of concentrated monovalent or bivalent unlabeled Nanobody. Mice were anesthetized with a mixture of 18.75 mg/kg ketamine hydrochloride (Ketamine 1000®, CEVA, Brussels, Belgium) and 0.5 mg/kg medetomidin hydrochloride (Domitor®, Pfizer, Brussels, Belgium) 10-15 minutes before pinhole SPECT acquisition.

MicroCT imaging was followed by pinhole SPECT on separate imaging systems. MicroCT was performed using a dual source CT scanner (Skyscan 1178, Skyscan, Aartselaar, Belgium) with 60 kV and 615 mA at a resolution of 83 µm. The total body scan time was 2 minutes. Image reconstruction was performed using filtered backprojection (Nrecon, Skyscan, Aartselaar, Belgium). Total body pinhole SPECT was performed at 60 minutes or 180 minutes post-injection (p.i.) using a dual headed gamma camera (e.cam¹⁸⁰ Siemens Medical Solutions, IL, USA), mounted with two multi-pinhole collimators (three pinholes of 1.5 mm in each collimator, 200 mm focal length, 80 mm radius of rotation). Images were acquired over 360 degrees in 64 projections of 10 s into 128×128 matrices resulting in a total imaging time of 14 minutes. The SPECT images were reconstructed using an iterative reconstruction algorithm (OSEM) modified for the three pinhole geometry and automatically reoriented for fusion with CT based on six ⁵⁷Co landmarks.

Image Analysis

Image viewing and quantification was performed using AMIDE Medical Image Data Examiner software. Ellipsoid regions of interest (ROIs) were drawn around the tumor and major organs. Uptake was calculated as the counts in the tissue divided by the injected activity counts and normalized for the ROI size (% IA/cm³). High-resolution image 3D-reconstructions were generated using OsiriX Imaging Software.

Biodistribution Analysis

Thirty minutes after microCT/SPECT acquisition, mice were sacrificed with a lethal dose of pentobarbital (Nembutal; CEVA). Tumor, kidneys, liver, lungs, muscle, spleen, lymph nodes, bone, heart, and blood were removed and weighed, and the radioactivity was measured using an automated γ-counter (Cobra II Inspector 5003; Canberra-Packard). Tissue and organ uptake was calculated as percentage of injected activity per gram of tissue (% IA/g), corrected for decay.

Immunofluorescence Stainings

Mice were injected intravenously with 500 µg Alexa-fluor647-labeled Nbs and intraperitoneally with 80 mg/kg pimonidazole [hypoxypore-1, HPI, Inc.] for hypoxia stainings. Two hours later, tumors were fixed in 4% paraformaldehyde, rehydrated overnight (20% sucrose) and sectioned (5 µm). Antibodies were: rat anti-F4/80/alexa-fluor488 (CI:A3-1, Serotec), F(ab')₂ donkey anti-rabbit/Cy3 JacksonImmuno). Pictures were acquired with a Plan-Neofluar 10×/0.30 or 20×/0.50 (Carl Zeiss) objective on a Zeiss Axioplan2 microscope with an Orca-R2 camera (Hamamatsu) and Smartcapture 3 software (Digital Scientific UK).

Activation of Immune Cells In Vitro and In Vivo

Mono- or bivalent α-MMR and BCII10 Nbs were added in varying concentrations to bone marrow-derived dendritic cells (BMDCs) or bone marrow-derived macrophages (BMDMs) (0.2 µg/ml, 2 µg/ml and 20 µg/ml for monovalent Nbs and 0.4 µg/ml, 4 µg/ml and 40 µg/ml for bivalent Nbs) for 24 hours in vitro in the presence or absence of LPS (10 ng/ml).

For assessment of the effect of α-MMR Nb in vivo, naïve mice and 13 days 3LL-R tumor-bearing mice were injected intravenously with 5 µg monovalent Nb+200 µg bivalent Nb.

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After 0 hours, 6 hours and 24 hours, blood serum was collected by heart puncture, incubated for 30 minutes at 37° C. and centrifuged (1000×g, 10 minutes).

Cytokines and chemokines were quantified in culture supernatants or blood serum with specific sandwich ELISAs for IL-10 (BD Biosciences), TNF (R&D Systems), CCL17 (R&D Systems), IL1Ra (R&D Systems) or CCL22 (R&D Systems) in accordance with the protocol provided by the manufacturer.

Generation of Anti-Human MMR and Anti-Human/Mouse MMR Cross-Reactive Nanobodies

The anti-human macrophage mannose receptor (MMR) and anti-human/mouse MMR cross-reactive nanobodies (Nbs) were isolated from an immune phage library in a similar way as described before.^(29, 30, 31) However, in order to generate cross-reactive Nbs, an alternating immunization schedule was carried out. An alpaca (*Vicugna pacos*) was immunized with 100 µg human MMR (R&D Systems #2534) followed by 100 µg mouse MMR (R&D Systems #2535) one week later. This alternating schedule was maintained for a total of 6 weeks and both proteins were mixed with the Gerbu adjuvant before injection. After immunization, blood was collected and the peripheral blood lymphocytes were isolated. mRNA was extracted from these cells using TRIzol (Invitrogen) and was reverse-transcribed with oligo(dT) and SuperScript II RT (Invitrogen), following the manufacturer's instructions. The gene sequences encoding the variable domains (VHHs) were PCR amplified, with the leader sequence specific CALL001 (5'-GTC CTG GCT CTC TTC TAC AAG G-3'; SEQ ID NO:252) and CH₂ exon specific CALL002 (5'-GGT ACG TGC TGT TGA ACT GTT CC-3'; SEQ ID NO:253) primers. After 1% agarose gel separation, the 600 bp fragment VHH-CH₂ fragment was isolated from gel and re-amplified using the nested primers A6E (5'-GAT GTG CAG CTG CAG GAG TCT GGR GGA GG-3'; SEQ ID NO:254) and PMCF (5'-CTA GTG CGG CCG CTG AGG AGA CGG TGA CCT GGG T-3'; SEQ ID NO:255) specific for the framework-1 and framework-4 regions, respectively. These PCR fragments were ligated into the phagemid vector pMECS, a variant of pHEN4,⁽⁵²⁾ after digestion with the PstI and NotI restriction enzymes. The pMECS differs from the pHEN4 in coding for a HA (YPYDVPDYGS; SEQ ID NO:256) and 6xhistidine tag fusion at the C-terminus of the Nb instead of a HA tag only fusion. Ligated material was transformed in freshly prepared *E. coli* TG1 cells and plated on LB plates with ampicillin. The colonies were scraped from the plates, washed and stored at -80° C. in LB-medium supplemented with glycerol (50% final concentration). Using M13VCS helper phage infection, the VHH library was expressed on phages. Specific Nanobody-phages were enriched by several consecutive rounds of in vitro selection on antigen coated to wells of microtiter plates (Nunc). For isolation of human/mouse MMR cross-reactive Nbs, screening was performed using human and mouse MMR alternately. Bound phage particles were eluted with 100 mM triethylamine (pH 11.0), immediately neutralized with 1 M Tris-HCl (pH 7.4) and used to infect *E. coli* TG1 cells. Individual colonies were picked and expression of recombinant Nanobody-M13 protein III by addition of 1 mM isopropyl-β-D-thiogalac-topyranoside (IPTG). The periplasmic extract of each clone was subsequently tested in ELISA for human MMR recognition with non-specific antigen coated wells serving as a negative control. Human/mouse MMR cross-reactive Nbs were also screened in a similar fashion against mouse MMR, only clones reactive with both human and mouse antigens were withheld as cross-reactive Nbs. Each ELISA was performed on plates coated with 1 µg/ml MMR in

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100 mM NaHCO₃ buffer pH=8.8. After coating the plates are washed with PBS+0.05% Tween-20 (PBST) and blocked for two hours with PBS+0.05% Tween-20+2% non-fat dry milk-powder (Nestle) (PBSM). The PE extracts are then incubated for 1 hour on the plate and then washed with PBST followed by 1 hour incubation of 0.5 µg/ml mouse anti-HA tag antibody (16B12, Covance) in PBSM. After washing with PBST, 1.5 µg/ml alkaline phosphatase conjugated anti-mouse antibody (Sigma) in PBSM in added to the plate for 1 hour followed by PBST washing. Finally, the ELISA is developed using 2 mg/ml alkaline phosphatase substrate (Sigma) in AP-buffer (100 mM NaCl, 50 mM MgCl₂, 100 mM Tris pH=9.5) and the optical density signal at 405 nm is measured.

Expression and Purification of Anti-Human MMR and Anti-Human/Mouse MMR Cross-Reactive Nanobodies

The pMECS-Nb plasmids of the clones that scored positive in ELISA were transformed into *E. coli* WK6 cells. These cells stop translation at the TAG codon and therefore express the Nbs without a phage protein fusion. Production of recombinant VHH was performed in shaker flasks by growing the bacteria in Terrific Broth supplemented with 0.1% glucose and ampicillin until an absorbance at 600 nm between 0.6 and 0.9 was reached. VHH expression was then induced with 1 mM IPTG for 16 hours at 28° C. After pelleting the cells, the periplasmic proteins were extracted by osmotic shock. This periplasmic extract was loaded on a nickel-nitrilotriacetic acid (Thermo Scientific), and after washing, the bound proteins were eluted in PBS with 500 mM imidazol. The eluted fraction was dialyzed to Vivaspin 2 centrifugal concentrators (Sartorius). The final purity of the protein was checked by SDS-PAGE. The final yield was determined from UV absorption at 280 nm using the calculated theoretical extinction coefficient of the VHH.

Example 1

TS/A Tumors are Highly Infiltrated with a Heterogeneous Population of Myeloid Cells Containing Distinct Granulocyte and Monocyte/Macrophage Subsets

To study the tumor-infiltrating myeloid compartment, we employed the Balb/c mammary adenocarcinoma model TS/A. Subcutaneous tumors contained a large CD11b⁺ fraction, indicating a high infiltration of myeloid cells (FIG. 1A). Interestingly, this CD11b⁺ population was heterogeneous and encompassed at least 7 subsets, which could be readily distinguished based on their differential expression of MHC class II and Ly6C (FIG. 1A). Ly6C^{hi}MHC II⁺ cells (Gate 1: FIG. 1A) were F4/80⁺CX₃CR1^{low}CCR2^{hi}CD62L⁺, did not express the granulocyte markers Ly6G or CCR3 and had a small size and granularity (FSC^{low}SSC^{low}), indicating that they were Ly6C^{hi} monocytes (FIGS. 1A, 1C and FIG. 6). The CD11b⁺MHC II⁺ cells in Gates 2-4 were reminiscent of macrophages, having an enlarged macrophage-like scatter and expressing high levels of F4/80 (FIGS. 1A, 1C). Remarkably, distinct subsets of tumor-associated macrophages (TAMs) were clearly distinguishable: Ly6C^{int}MHC II^{hi} (Ly6C^{int} TAMs, Gate 2), Ly6C^{low}MHC II^{hi} (MHC II^{hi} TAMs, Gate 3) and Ly6C^{low}MHC II^{low} (MHC II^{low} TAMs, Gate 4). The majority of Ly6C^{low}MHC II⁺ cells were CCR3⁺CX₃CR1⁻ eosinophils (Gate 5: FIG. 1A and Gate E: FIG. 6). However, Ly6C^{low}MHC II⁺ cells also consisted of CCR3⁻CX₃CR1^{hi} (Gate 2: FIG. 6) and CCR3⁻CX₃CR1^{hi} (Gate 3: FIG. 6) cells, the latter possibly resembling Ly6C^{low}CX₃CR1^{hi} monocytes. However, the majority of these CX₃CR1^{hi} cells did not have a monocyte scatter, suggesting they were TAMs (FIG. 6). This

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suggests that Ly6C^{low} monocytes were not present in significant amounts in these tumors. Finally, TS/A tumors were also infiltrated with CCR3⁺Ly6C^{int} eosinophils (Gate 6: FIG. 1A), and Ly6G^{hi} neutrophils (Gate 7: FIG. 1A).

Interestingly, the relative percentages of these distinct myeloid subpopulations dramatically changed as tumors progressed (FIG. 1B). Within the TAM compartment, the percentage of Ly6C^{int} TAMs decreased, while the Ly6C^{low}MHC II^{low} TAM subset became gradually more prominent, reaching up to 60% of the myeloid tumor-infiltrate in large tumors (>10 mm).

Example 2

Ly6C^{hi} Monocytes are the Precursors of all TAM Subsets in TS/A Tumors

Macrophages typically derive from circulating blood-borne precursors such as monocytes. The presence of Ly6C^{hi}, but not Ly6C^{low}, monocytes in TS/A tumors suggested that the former could be more efficiently recruited to tumors and function as the TAM precursor. To investigate this, we selectively labeled Ly6C^{hi} or Ly6C^{low} monocyte subsets in vivo with fluorescent latex beads, using a previously described procedure.^(11, 12) This method has been validated to stably label the respective monocyte subsets for 5 to 6 days in naïve mice. Hence, TS/A was injected after Ly6C^{low} or Ly6C^{hi} monocyte labeling and tumors were collected 6 days pi. No appreciable numbers of tumor-infiltrating latex⁺monocytes were observed when applying the Ly6C^{low} labeling strategy (FIG. 2A). In contrast, Ly6C^{hi} labeling resulted in the detection of a significant fraction of CD11b⁺latex⁺ monocytes, illustrating that Ly6C^{hi} monocytes are the main tumor-infiltrating monocyte subset. With this approach, latex⁺ cells could be detected up to 19 days post tumor injection (FIG. 2B), allowing a follow-up of the monocyte progeny in the course of tumor growth. At day 6, latex⁺Ly6C^{hi} monocytes had differentiated into latex⁺Ly6C^{int} TAMs, and to some extent also into latex⁺MHC and latex⁺MHC II^{low} TAMs (FIG. 2B). From day 12 onward, the majority of latex⁺Ly6C^{hi} monocytes had converted into latex⁺MHC II^{hi} and latex⁺MHC II^{low} TAMs. Together, these data demonstrate that all TAM subsets can be derived from Ly6C^{hi} monocytes.

Example 3

Ly6C^{int}, MHC II^{hi} and MHC TAMs have Distinct Differentiation Kinetics and Turnover Rates

To determine the turnover rate and differentiation kinetics of the monocyte/TAM subsets, BrdU was administered continuously to tumor-bearing animals and its incorporation was measured at consecutive time points. Tumor-infiltrating Ly6C^{hi} monocytes quickly became BrdU⁺, reaching plateau values after 48 hours of BrdU administration (FIG. 2D). This indicates a rapid monocyte turnover rate and/or proliferation of monocytes inside tumors. Remarkably, intratumoral Ly6C^{hi} monocytes were Ki67⁺, suggesting a proliferative potential (FIG. 2C). In contrast, TAMs were non-proliferating (Ki67⁻) and hence unable to directly incorporate BrdU. Therefore, BrdU⁺ TAMs must differentiate from BrdU⁺ monocytes, resulting in a lag phase of BrdU positivity. Indeed, only a minor fraction of MHC II^{hi} and MHC II^{low} TAMs were BrdU⁺ upon 24 hours BrdU administration (FIG. 2D). However, compared with these subsets, Ly6C^{int} TAMs incorporated BrdU at a faster rate, with a higher percentage being BrdU⁺ already at 24 hours. These results suggest that

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monocytes first give rise to Ly6C^{int} TAMs, which then differentiate into MHC II^{hi} and MHC II^{low} TAMs. MHC II^{hi} and MHC II^{low} TAMs incorporated BrdU slowly and with similar kinetics, arguing for a comparable and low turnover rate.

Example 4

MHC II^{hi} and MHC II^{low} TAMs Differ at the Molecular Level

Efforts have been made before to characterize TAMs at the molecular level.^(13, 14) We characterized the distinct TAM subsets at the gene and protein level. The gene expression of sorted MHC II^{hi} and MHC II^{low} TAMs (FIG. 7A) was analyzed via qRT-PCR (Table 1). Ly6C^{int} TAMs, constituting only a minor fraction in larger tumors, were not included in this analysis. Interestingly, when comparing MHC II^{hi} with MHC II^{low} TAMs (Table 1 hi/low), M2-associated genes such as Arg1 (Arginase-1), Cd163, Stab1 (Stabilin-1) and Mrc1 (MMR) were higher expressed in the MHC II^{low} subset. In contrast, more M1-type, pro-inflammatory genes such as Nos2 (iNOS), Ptgs2 (Cox2), Il1b, Il6 and Il12b were up-regulated in MHC II^{hi} TAMs. This differential activation state was also reflected at the protein level. Membrane expression of the M2 markers macrophage mannose receptor (MMR), macrophage scavenger receptor 1 (SR-A) and IL-4R α were clearly higher on MHC II^{low} TAMs, while the M1-associated marker CD11c, was only expressed on MHC II^{hi} TAMs (FIG. 1C). Moreover, while arginase activity was observed in both TAM subsets, it was significantly higher for MHC II^{low} TAMs (FIG. 3A). In the same vein, TNF α , which has previously been reported to associate with a M2 phenotype in tumors,^(15, 16) was produced by both TAM subsets, but a significantly higher percentage of MHC II^{low} TAMs were found to be TNF α ⁺ (FIG. 3B). While iNOS protein was not detected in freshly isolated TAMs, it could be induced by IFN- γ and/or LPS stimulation (FIG. 3C). Interestingly, IFN- γ or LPS induced iNOS more efficiently in MHC II^{hi} TAMs, with a higher fraction of these cells becoming iNOS⁺. Together, these data indicate that the identified TAM subsets have a differential activation state, with MHC II^{low} TAMs being more M2-oriented.

TAM subsets also showed a markedly distinct chemokine expression pattern (Table 1). Notably, mRNAs for chemokines typically involved in lymphocyte attraction, such as Ccl5, Cx3cl1, Cxcl11, Cxcl10, Cxcl9 and the CCR4 ligands Ccl17 and Ccl22 were up-regulated in MHC II^{hi} TAMs. In contrast, mRNAs for monocyte/macrophage chemoattractants, such as Ccl6, the CCR2 ligands Ccl7, Ccl2 and Ccl12 and the CCR5/CCR1 ligands Ccl4, Ccl3 and Ccl9 were significantly higher in MHC II^{low} TAMs. Furthermore, at the protein level, a differential expression of the chemokine receptors CX₃CR1 and CCR2 was observed, with MHC II^{hi} TAMs being CX₃CR1^{hi}CCR2⁻, while MHC II^{low} TAMs were CX₃CR1^{low}CCR2⁺ (FIG. 1C).

Both TAM subsets expressed many potentially pro-angiogenic genes, including Vegfa, Mmp9, Pgf, Spp1 and cathD (Table 1). However, several angiostatic factors such as angpt2, Cxcl9, Cxcl10 and Cxcl11 were up-regulated in the MHC II^{hi} fraction. One of the most differentially expressed genes (higher in MHC II^{low} TAMs) was Lyve1.

We conclude that MHC II^{hi} and MHC II^{low} TAMs have a distinguishing profile of molecules involved in inflammation (M1/M2), chemotaxis and angiogenesis.

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Example 5

MHC II^{low} TAMs are Enriched in Regions of Hypoxia, while MHC II^{hi} TAMs are Mainly Normoxic

Tumors often harbor regions of hypoxia, a factor which is known to influence macrophage function.⁽⁹⁾ To visualize hypoxia in TS/A tumors, tumor-bearing mice were injected with pimonidazole (Hypoxyprom-1, HP-1) and tumor sections were stained for hypoxic adducts and blood vessels. FIG. 4A shows that tumors indeed contained a large number of hypoxic cells, primarily in regions with a less developed vasculature. Interestingly, staining sections for HP-1, CD11b and MHC II demonstrated that many CD11b⁺MHC II⁻ cells (which in large tumors are mainly MHC II^{low} TAMs) were HP-1⁺ (FIG. 4B). Interestingly however, the majority of CD11b⁺MHC II⁺ cells were HP-1⁻. This indicates that while a significant fraction of MHC II^{low} TAMs resided in hypoxic areas, MHC II^{hi} TAMs were mainly normoxic. Importantly, HP-1 adducts could also be detected through intracellular flow cytometry on freshly isolated TAMs. Again, the highest signal was seen in MHC II^{low} TAMs, confirming they were the most hypoxic TAM subset (FIG. 4C).

A consequence of MHC II^{low} TAMs being in hypoxic regions should be a reduced access to blood-transported molecules. To test this, fluorescent latex particles were injected iv in tumor-bearing mice. 1 to 2 hours later a fraction of tumor-associated CD11b⁺ cells were found to be latex⁺ (FIG. 8A). However, latex uptake was not equal in all TAM subsets. Indeed, in relative terms, MHC II^{low} TAMs phagocytosed less latex than monocytes and other TAM subsets. This was not due to an inherently reduced phagocytic capacity of MHC II^{low} TAMs, since the latter showed the highest phagocytic latex uptake in vitro (FIG. 8B). These data suggest that the reduced in vivo latex uptake of MHC II^{low} TAMs was due to a restricted access to latex particles which further substantiates the enrichment of MHC II^{low} TAMs in hypoxic regions.

Example 6

MHC II^{low} TAMs Show a Superior Pro-Angiogenic Activity In Vivo

Hypoxia initiates an angiogenic program.⁽¹⁷⁾ In addition, our gene profiling revealed the expression of angiogenesis-regulating molecules in TAMs. To directly test the pro-angiogenic activity of both TAM subsets in vivo, we employed the chorioallantoic membrane (CAM) assay. Sorted MHC II^{hi} or MHC II^{low} TAMs were implanted on developing CAMs, while BSA or rhVEGF served as negative and positive controls, respectively. rhVEGF induced the outgrowth of allantoic vessels specifically directed towards the implants (FIG. 5A). Interestingly, compared with BSA controls, the presence of MHC II^{hi} or MHC II^{low} TAMs significantly increased the number of implant-directed vessels, demonstrating a pro-angiogenic activity for both TAM subsets. However, the vessel count for implants containing MHC II^{low} TAMs was on average two-fold higher than with MHC II^{hi} TAMs. These data show that MHC II^{low} TAMs had a superior pro-angiogenic activity in vivo.

Example 7

TAMs are Poor Antigen-Presenters, but can Efficiently Suppress T-Cell Proliferation

We wondered whether the TAM subsets were able to process internalized antigens and activate T cells. Both TAM

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subsets took up and processed DQ-Ovalbumin (DQ-OVA) at 37° C. However, examining DQ-OVA processing at consecutive time points indicated that processing naïve more slowly in the MHC II^{low} fraction (FIG. 9). To investigate whether TAMs could directly activate naïve T cells, a mixed leukocyte reaction (MLR) assay was used. Hereto, sorted MHC II^{hi} or MHC II^{low} TAMs were cultured with purified allogeneic C57BL/6 CD4⁺ or CD8⁺ T cells. Sorted splenic CD11c^{hi}MHC II^{hi} conventional DCs (cDCs) (FIG. 7B) were used as a reference T-cell-stimulating population.⁽¹⁸⁾ Compared with cDCs, MHC II^{hi} or MHC II^{low} TAMs induced poor proliferation of allogeneic CD4⁺ or CD8⁺ T cells (FIG. 5B), suggesting a limited antigen-presenting capacity or, alternatively, a T-cell suppressive capacity that overrules antigen presentation.

To investigate the latter possibility, T cells were polyclonally activated in the presence of TAMs or cDCs. Interestingly, as opposed to cDCs, both MHC II^{hi} and MHC II^{low} TAMs equally suppressed anti-CD3-induced T-cell proliferation in a dose-dependent manner (FIG. 5C). In an attempt to identify the suppressive molecules responsible for TAM-mediated suppression, inhibitors of iNOS (L-NAME) and arginase (N or Noha) were added to the co-cultures (FIG. 5D). Blocking iNOS significantly reduced T-cell suppression by MHC II^{hi} TAMs, demonstrating a role for nitric oxide in its suppressive mechanism. In contrast, iNOS inhibition only had a minor effect on the suppressive potential of MHC II^{low} TAMs, showing that both subsets employ different T-cell suppressive mechanisms.

Example 8

Similar TAM Subsets in Other Tumor Models

Interestingly, the TAM subsets identified in TS/A tumors, were also present in other tumor models. Both in the Lewis Lung Carcinoma (LLC) model and in the mammary carcinoma model 4T1, MHC II^{hi} and MHC II^{low} TAMs could be identified (FIG. 13A). Furthermore, as in TS/A, typical M2 markers such as MMR and IL4Rα were higher expressed on MHC II^{low} TAMs, while M1 markers such as CD11c were higher on MHC II^{hi} TAMs (FIG. 13B). This indicates that our initial findings in TS/A are not restricted to a single tumor model or even to a single carcinoma type (mammary vs. lung carcinoma). The dynamics of TAM subsets in the LLC model resembled that of TS/A, with MHC II^{low} TAMs accumulating over time and forming the majority of myeloid cells in established tumors (FIG. 13C, LLC). However, 4T1 tumors did not adhere to this trend and instead MHC II^{hi} TAMs accumulated as tumors progressed (FIG. 13C, 4T1). These data indicate that the accumulation of TAM subsets over time can vary from one tumor type to another, which possibly reflects differences in tumor architecture. Therefore, these findings provide a rationale for classifying tumors based on the relative percentage of TAM subsets (with tumor volume taken into account). This might be useful for devising a tailored therapy and/or as a prognostic factor.

Example 9

Nanobodies Against the Macrophage Mannose Receptor (CD206-MMR)

As outlined in the Examples above, TAMs can adopt different phenotypes and functional specializations. For example, TAMs located in hypoxic tumor regions were found to be extremely pro-angiogenic, suggesting that they play an

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important role in tumor vascularization. Interestingly, we have identified CD206 (macrophage mannose receptor) as a membrane marker which is specifically expressed on this tumor-promoting TAM subset. Anti-CD206 (anti-MMR) nanobodies, which are the smallest available antigen-binding entities, were created (see also Example 14) in order to target these cells in vivo. It was shown that the newly created anti-CD206 Nbs bind strongly to TAMs, but not to other myeloid cell types such as monocytes and granulocytes or any other tumor resident cells. These and other nanobodies against any of the markers of Table 1 are used for non-invasive imaging of TAMs using SPECT/Micro-CT. These nanobodies are also used to create immunotoxins for the therapeutic targeting of these cells in pre-clinical tumor models or for antibody-directed enzyme prodrug therapies (ADEPT).

Example 10

In Vivo Imaging Using Macrophage Mannose Receptor Nanobodies

In a next step, we performed in vivo imaging using Macrophage Mannose Receptor (MMR) targeting nanobodies. The nanobodies were labeled at their hexahistidine-tail with ^{99m}Tc at elevated temperatures by tricarbonyl-chemistry. Purified, ^{99m}Tc -labeled Nanobodies were injected intravenously in mice and total body scans were made using pinhole SPECT and micro-CT.

The first step in the in vivo evaluation was the study of the biodistribution in healthy mice. This allows to evaluate physiological sites of specific accumulation and to determine the pharmacokinetic properties of the imaging probes. MMR nanobodies show uptake in organs such as lungs, spleen and liver. The blood clearance is fast with less than 1% IA (injected activity)/ml remaining in blood at 1 hour 30 minutes post injection. We also tested MMR nanobodies in MMR knock-out mice where the uptake in liver and spleen dropped below 1% IA/g (FIG. 11). These data indicate that the accumulation in organs such as liver and spleen is related to MMR expression and therefore specific. Only the accumulation in lungs appears to be MMR-unrelated.

Next, ^{99m}Tc -labeled MMR Nanobodies and a control Nanobody recognizing a target not present in mice (the cAb-BcII10 nanobody, raised against subunit 10 of the β -lactamase BcII enzyme of *Bacillus cereus*) were inoculated in TS/A tumor-bearing mice. Uptake of the MMR Nanobody in liver, spleen, lungs, kidneys and blood was similar as before (FIG. 12), whereas accumulation of the control Nanobody was below 1% IA/g for all organs except for lungs and kidneys. Interestingly, the MMR Nanobody showed significant accumulation in the subcutaneous TS/A tumor (>2.5% IA/g), whereas the uptake of the control Nanobody in the subcutaneous tumor had dropped below 0.5% IA/g at 1h30 post injection.

Example 11

TAM Targeting Using Anti-CD206 Nb-Toxins

Anti-CD206 Nbs are covalently linked to a protein toxin for TAM cell killing. Candidate toxins are the diphtheria toxin or the *Pseudomonas* exotoxin. It is investigated whether Nb-toxin conjugates are able to induce TAM cell death both in vitro and in vivo. Next, the effect of Nb-toxin treatment on tumor growth is assessed. For this, different injection schemes and doses are evaluated, ideally obtaining tumor regression coupled to a low overall toxicity. Further, it is

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investigated whether in vivo TAM depletion results in reduced tumor angiogenesis. This is done by immunohistochemically counting the number of blood vessels in tumors of Nb-toxin treated or untreated mice.

Alternatively, TAM killing might alleviate immune suppression or induce an inflammatory environment favoring the development of anti-tumor immunity. Thereto, it is investigated whether Nb-toxin treatment expands tumor-infiltrating T cells (TILs). The activation of TILs is assessed by evaluating the expression of certain membrane markers and through intracellular measurement of cytokine production. CD8⁺ cytotoxic TILs are purified and their tumor killing potential is directly assessed in vitro. The impact of anti-tumor immunity is also evaluated by repeating the Nb-toxin treatment in Rag2^{-/-} or SCID mice, which do not have functional T or B cells.

Example 12

Targeting Tumors Using an Anti-CD206 Nb-Enzyme/Prodrug Strategy

The observation that CD206 is expressed on TAMs from several independent tumor models, makes it a potential tumor-targeting marker for a variety of different cancers. CD206 is therefore an interesting candidate for developing antibody-directed enzyme prodrug therapies (ADEPT). In ADEPT an antibody is coupled to an enzyme which is able to convert a prodrug into a cytotoxic drug. We have previously proven that this also works with the Nb format.⁽²⁵⁾ Anti-CD206 Nbs can, for example, be coupled to β -lactamase, an enzyme which is able to release phenylenediamine mustard from the prodrug 7-(4-carboxybutanamido) cephalosporin mustard. Anti-CD206 Nb-enzyme conjugates can be injected in tumor-bearing mice, subsequently allowing clearance of unbound Nbs after which the prodrug is administered. This will result in a high toxicity at the tumor site, killing TAMs but also other bystander tumor cells, while having a low overall toxicity in the animal. We evaluate the efficacy of anti-CD206 Nb enzyme-prodrug therapies for inducing tumor regression in our preclinical tumor models.

Example 13

MMR as a Marker for the Differential Targeting of Tam Subsets In Vivo

In the above Examples, it was shown that in tumor single cell suspensions, MMR was differentially expressed between MHC II^{hi} and MHC II^{low} TAMs, as assessed by flow cytometry using anti-MMR monoclonal antibodies. In addition, MMR was not/poorly expressed on CD11b⁻ cells, granulocytes, monocytes and Ly6C^{int} TAMs in the TS/A mouse mammary carcinoma model (FIG. 14). We next set out to investigate MMR expression patterns in tumor sections. TS/A mammary carcinoma sections were triple-stained for MMR (red), CD11b (blue) and MHC II (green) (FIG. 15). MMR and CD11b staining almost completely co-localized, showing that MMR cells were indeed TAMs. Interestingly however, MMR expression poorly co-localized with CD11b⁺MHC II⁺ cells (the majority corresponding to MHC II^{hi} TAMs), indicating that MMR staining was mainly restricted to MHC II^{low} TAMs. Therefore, MMR can be used for differentially targeting MHC II^{hi} and MHC II^{low} TAMs on tumor sections. Together with our flow cytometric results this indicates that MMR can be an interesting marker for specifically targeting MHC II^{low} TAMs in vivo.

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Example 14

Generation of Anti-MMR Monovalent and Bivalent Nanobodies

Nanobodies (Nb) were raised against the recombinant extracellular portion of MMR (α -MMR Nb), as described in the Materials and Methods (see also Example 9; Table 4). The binding characteristics of the monovalent anti-MMR nanobodies were compared using surface Plasmon resonance measurements (Table 5). Nanobody clone 1 demonstrated an eight-fold higher apparent affinity for immobilized recombinant MMR compared to nanobody clone 3 ($K_D=2.31\times 10^{-8}$ M versus 1.91×10^{-7} M, respectively), and became hence the nanobody of choice for the remaining of this study. In addition, SPR competition studies demonstrated that pretreatment with nanobody clone 1 does not preclude nanobody clone 3 binding, and vice versa, suggesting that anti-MMR Nb clone 1 and Nb clone 3 bind to non-overlapping epitopes (data not shown). Further, bivalent nanobodies were constructed by linking two anti-MMR nanobody 1 entities using $(G_4S)_3$ (GGGGSGGGSGGGGS; SEQ ID NO:121), llama IgG2 hinge (AHHSEDPSSKAPKAPMA; SEQ ID NO:122) or human IgA hinge (SPSTPPTSPSTPPAS SEQ ID NO:123) linkers. These bivalent anti-MMR molecules showed a five-fold higher avidity compared to the monovalent clone 1 nanobody, which can be attributed largely to three-fold increase in K_D . The different linkers used for bivalent nanobody construction did not seem to have a significant effect on the affinity of the molecules for the MMR antigen. As a negative control nanobody in all experiments, we consistently used α -BCII10 Nb, which is a binder of the β -lactamase BCII enzyme of *Bacillus cereus*.

Example 15

Ex Vivo Characterization of Anti-MMR Nanobodies

To investigate whether the anti-MMR Nb could bind to TAMs ex vivo, single cell suspensions were made of subcutaneous TS/A tumors and flow cytometric analyses were performed (FIG. 16). The anti-MMR Nb bound to a subset of CD11b⁺ cells, but not to CD11b⁻ cells (FIG. 16A). Within the CD11b⁺ fraction, anti-MMR Nb did not bind to monocytes (FIG. 16B, gate 1), granulocytes (Gate 5) and only very weakly to Ly6C^{int} TAMs (gate 2). Staining was therefore restricted to MHC II^{hi} (gate 3) and MHC II^{low} TAMs (gate 4), with the latter subset binding anti-MMR Nb to a much greater extent. These results are therefore in line with our previous observations using anti-MMR monoclonal antibodies. We conclude that in ex vivo tumor suspensions, the anti-MMR Nb stained mature TAMs and more intensely the MHC II^{low} subset.

Example 16

Assessment of the Biodistribution and Specificity of Anti-MMR Nanobody Clone 1 and its Bivalent Derivative in Naive Mice Using Pinhole SPECT/Micro-CT Analysis

Next, we wished to assess whether the anti-MMR Nb clone 1 could be used for targeting and imaging of MMR-expressing cells in vivo. In first instance, this was investigated in naive mice. To this end, anti-MMR monovalent Nb were labeled with ^{99m}Tc and injected intravenously in naive C57BL/6 mice. Three hours post injection, total-body scans

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were acquired using pinhole SPECT and micro-CT (FIG. 17), images were quantified and tracer uptake expressed as percentage injected activity per gram cubic centimeter (% IA/cm³) (Table 6). To ascertain the specificity of the anti-MMR Nb and to prove that any potential targeting was not due to aspecific retention, anti-MMR Nb were also injected in naive C57BL/6 MMR^{-/-} mice. In MMR^{-/-} mice, SPECT/micro-CT images show a high tracer uptake in the kidneys and urinary activity in the bladder, indicative of renal clearance, but only low background-level retention is seen in other organs (FIG. 17, Table 6). The only exception were the lungs, suggesting that lung-targeting was aspecific. In contrast, WT mice showed an increased retention of the anti-MMR Nb in several organs, including heart, bone, spleen and liver, with the latter two showing the most intense signals (FIG. 17). These results indicate that the anti-MMR monovalent Nb has a high in vivo specificity and can efficiently target organs such as the liver and spleen. A similar experiment was performed with the different bivalent anti-MMR Nb constructs, all of which showing an even increased uptake in the liver as compared to the monovalent molecule and a concomitant reduction in clearance via the kidneys (Table 7). Again, retention of bivalent anti-MMR Nb in all organs, except the lung, is MMR-specific and is absent in MMR^{-/-} mice. As was expected, retention of the control cAbBCII10 Nb is very low in all organs, resulting in a massive clearance via the kidneys (Table 7).

Example 17

Tumor-Targeting Potential and Specificity of Anti-MMR Nanobodies

Next, we set out to investigate whether the anti-MMR Nb could be used to target TAMs in vivo. Hereto, ^{99m}Tc-labeled anti-MMR Nbs were injected intravenously in TS/A (Balb/c) and 3LL-R (C57BL/6) tumor-bearing mice and SPECT/micro-CT and ex vivo dissection analyses were performed. ^{99m}Tc-labeled cAbBCII10 Nbs were used as negative controls. In addition, to further ascertain the specificity of tumor uptake, 3LL-R tumors were also grown in C57BL/6 MMR^{-/-} mice. In these mice, 3LL-R tumors grew progressively and the distinct TAM subsets remained present as assessed by flow cytometry (data not shown). Interestingly, as observed by SPECT/micro-CT imaging, both TS/A and 3LL-R tumors showed a clear uptake of anti-MMR Nb, which was significantly higher than tumor uptake of cAbBCII10 Nb (FIGS. 18 and 19). These findings were confirmed through ex vivo dissection analysis, where the activity in the tumor and organs was assessed and expressed as injected activity per gram (% IA/g): TS/A tumor uptake was $3.02\pm 0.10\%$ IA/g for anti-MMR Nb and $0.40\pm 0.03\%$ IA/g for cAbBCII10 (Table 8); 3LL-R tumor uptake was $3.02\pm 0.19\%$ IA/g for anti-MMR Nb and $0.74\pm 0.03\%$ IA/g for cAbBCII10 (Table 9). Importantly, in 3LL-R tumor-bearing MMR^{-/-} mice, tumor uptake of anti-MMR Nb was reduced by ten-fold ($0.33\pm 0.03\%$ IA/g, Table 9), showing that targeting in WT mice was receptor-specific.

Example 18

Blocking of Extratumoral Binding Sites by Excess Monovalent or Bivalent Anti-MMR Nb

Both in the TS/A and 3LL-R model, ^{99m}Tc-labeled anti-MMR Nb accumulates to a higher extent in liver and spleen than in the tumor. Therefore, we sought for ways to minimize binding of labeled tracer in these extratumoral sites, while

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preserving tumor targeting. In first instance, we co-injected an eighty-fold excess of cold unlabeled anti-MMR Nb and subsequently evaluated the biodistribution of ^{99m}Tc -labeled anti-MMR Nb. This strategy results in a strongly reduced accumulation of labeled Nb in all organs, except for the tumor, resulting in a similar level of specific uptake in tumor and liver (FIG. 20). Next, we hypothesized that the inherently enhanced biodistribution of bivalent anti-MMR Nb to the liver and its enhanced in vivo retention (lower clearance via the kidneys) could be exploited to block the extratumoral binding sites more efficiently. To this end, we co-injected ^{99m}Tc -labeled anti-MMR Nb with a twenty-fold excess of cold bivalent anti-MMR and assessed the specific uptake of labeled Nb in distinct organs. Remarkably, while the retention of monovalent anti-MMR in all organs is reduced to the aspecific background level seen with the control Nb cAb-BCII10, the uptake in tumors is only slightly diminished (FIG. 21). As a result, the specific uptake of labeled anti-MMR Nb is highest in the tumor.

Example 19

The Relative Abundance of TAM Subsets Correlates with Tumor Aggressiveness

To assess whether the relative abundance of TAM subsets correlates with tumor aggressiveness, we injected high and low malignant 3LL lung carcinoma variants and evaluated the TAM subset distribution in the corresponding tumors. 3LL-R lung carcinoma cells establish rapidly growing tumors upon subcutaneous inoculation, reaching a tumor volume of about 1000 mm³ within 12 days (FIG. 22). In these tumors, the MHC II^{high} TAM subpopulation, which is located in normoxic regions, is outnumbered by the MHC II^{low} subset (FIGS. 22 and 23). In contrast, 3LL-S tumors grow much slower (1000 mm³ within about 35 days) and are dominated by the MHC II^{high} TAM subset (FIG. 22). A similar observation is made when comparing fast growing T241 fibrosarcoma tumors with slow growing T241-HRG tumors (data not shown). Together, these data indicate that the relative abundance of TAM subsets can be prognostic for tumor aggressiveness.

Example 20

Evaluation of the Anti-MMR-PE38 Immunotoxin

The anti-MMR Nb clone 1 was fused to the *Pseudomonas* exotoxin A as described in Materials and Methods, creating an MMR-specific immunotoxin. It was shown that the recombinant production of this immunotoxin results in a functional toxic moiety, with the ability to kill cancer (3LL-R, 3LL-S) and macrophage cell lines (J774) in vitro (data not shown). In vivo administration of the toxin does not result in lethality, even at the highest dose used (data not shown). Further, the ability of the immunotoxin to specifically eliminate MMR-positive cells in vivo is assessed, in particular MMR⁺MHC II^{low} TAM in tumors, and the consequences of TAM subset elimination for tumor characteristics (growth, metastasis, vessel density, vessel functionality, . . .) is evaluated.

Example 21

 α -MMR Nb Clone 1 Targets Hypoxic Tumor-Associated Macrophages In Vivo

Having established that α -MMR Nb c11 specifically targeted MMR cells in tumors, we wished to ascertain whether

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this was due to TAM targeting. Previous work showed that CCR2-deficiency can result in a significant decrease in TAM infiltration with only a minimal effect on tumor growth, resulting from the compensatory influx of tumor-promoting neutrophils.^(45, 46) To investigate whether CCR2-deficiency affected the numbers of TAMs and in particular MHC II^{low} TAMs in our model, flow cytometric analyses were performed on single-cell suspensions of equally sized s.c. 3LL-R tumors grown in WT or CCR2-KO mice. This showed that CCR2-deficiency led to a dramatic reduction in the number of MHC II^{low} TAMs, while infiltration of Ly6G⁺MMR⁺ neutrophils was significantly increased (FIG. 24A). Next, we compared the tumor-uptake of ^{99m}Tc -labeled α -MMR Nb c11 injected in WT vs CCR2-KO 3LL-R tumor-bearing mice. ^{99m}Tc -labeled α -MMR Nb showed a similar biodistribution in the organs/tissues of CCR2-KO vs WT tumor-bearers (Table 10). Importantly however, uptake of ^{99m}Tc -labeled α -MMR Nb was significantly reduced in CCR2-KO tumors: $2.97 \pm 0.22\%$ IA/g in WT vs $1.83 \pm 0.1\%$ IA/g in CCR2-KO tumors (FIG. 3B). This indicates that TAMs residing in solid tumors are indeed targets of α -MMR Nbs in vivo.

Since MHC II^{low} MMR⁺ TAM were shown to associate with hypoxic regions, we next assessed whether α -MMR Nbs preferentially label hypoxic TAM in vivo. Hereto, AF647-coupled α -MMR Nbs were injected i.v. in s.c. 3LL-R WT or MMR-KO tumor-bearing mice. Two hours later, tumors were collected, sectioned and stained for the hypoxia marker pimonidazole (hypoxyprobe) and the macrophage marker F4/80. Interestingly, AF647 fluorescence almost completely co-localized with F4/80 staining in WT tumors, but was absent from MMR-KO tumors (FIG. 24C). In addition, the majority of AF647(bright) cells were located in hypoxic areas and stained with pimonidazole (FIGS. 24C and 24D). These results convincingly show that α -MMR Nbs can target hypoxic tumor regions in vivo, where they bind to the residing MMR macrophages.

Example 22

Strategies for Increasing the Tumor-to-Tissue Ratio of ^{99m}Tc -Labeled α -MMR Nb c11

A methodology for the specific in vivo targeting of a tracer to TAMs, but not to other sites in the body, could be of important diagnostic and therapeutic significance. However, both in the TS/A and 3LL-R model, ^{99m}Tc -labeled anti-MMR Nb accumulates to a higher extent in liver and spleen as compared to tumor. Therefore, we aimed to minimize binding of labeled tracer in these extratumoral sites, while preserving tumor targeting. The efficient tumor targeting potential of nanobodies is thought to be a direct result of their small size. To investigate this, a series of larger bivalent Nbs were created (FIG. 25A). First, α MMR- α MMR bivalent Nbs were made by cloning three different peptide linkers with increasing proline content (glycineserine linker, part of the llama IgG2c hinge or part of the human IgA hinge) between two Nb c11 sequences (as described in Example 14). All these bivalent Nbs showed a five-fold higher avidity compared to the monovalent Nb c11, which can be largely attributed to a three-fold increase in K_D (Table 5) and displayed a very similar in vivo biodistribution (Table 7). In addition, using the llama IgG2c linker, α MMR-BCII10 bispecific Nbs and BCII10-BCII10 bivalent Nbs were generated and their in vivo biodistribution was evaluated in TS/A and 3LL-R tumor-bearing mice. Interestingly, α MMR-BCII10 and especially α MMR- α MMR Nbs showed a significantly enhanced targeting of liver and spleen, but a dramatically reduced targeting of

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tumor, as compared to monovalent α -MMR Nbs (FIG. 25B). Hence, these bivalent Nbs seem to possess desirable features to efficiently block extratumoral binding sites while preserving intratumoral binding sites. To test this, we co-injected ^{99m}Tc -labeled monovalent α -MMR Nb with a twenty-fold molar excess of unlabeled bivalent α MMR- α MMR Nb and assessed the specific uptake of labeled Nb in distinct organs. While the retention of monovalent ^{99m}Tc -labeled α -MMR Nb is reduced in all organs to the aspecific background level seen with Nb BCII10, the uptake in tumors is only slightly diminished (FIG. 25C). As a result, the tumor-to-tissue ratio of labeled α -MMR Nb is dramatically increased and tracer uptake is highest in the tumor. This allowed the tumor to be clearly distinguishable in SPECT/micro-CT imaging of mice bearing subcutaneous tumors (FIGS. 26A and 26B). Importantly, very similar imaging data were obtained when TS/A tumors were grown orthotopically in the mammary fat pad (FIGS. 5C and 5D), for which the presence of the two main TAM subsets as described above (Example X). Finally, imaging studies were performed in transgenic MMTV-PyMT mice, which spontaneously develop mammary tumors.⁽³³⁾ Hereto, a mouse bearing multiple macroscopic tumors was consecutively imaged (48-hour intervals to allow complete elimination and decay of the ^{99m}Tc tracer) with either ^{99m}Tc -labeled α -MMR Nb, ^{99m}Tc -labeled BCII10 Nb or ^{99m}Tc -labeled α -MMR Nb co-injected with unlabeled bivalent α MMR- α MMR Nb. When ^{99m}Tc -labeled α -MMR Nb was injected alone, tumors were not easily distinguishable due to high extratumoral uptake (FIG. 27A). However, co-injecting unlabeled bivalent α MMR- α MMR Nb minimalized extratumoral Nb retention and resulted in tracer uptake in the most prominent macroscopic nodules as seen via high-resolution 3D CT reconstructions (FIG. 27B). Notably, FACS analysis showed that for all three selected tumors highlighted in FIG. 6B, distinct TAM subpopulations were present, whereby MMR expression was highest on the MHC II^{low} TAMs (FIG. 27C).

Example 23

Effect of Mono- and Bivalent α -MMR Nb c11 on Immune Cell Activation

Monoclonal anti-MMR antibodies are known to potentially activate macrophages and DCs.⁽⁴⁷⁾ To assess whether mono- or bivalent α -MMR Nb c11 elicits a response, Nbs were added in varying concentrations to bone-marrow derived DCs (BMDCs) or macrophages (BMDMs) in vitro or were injected at a high dose in vivo. Monovalent α -MMR Nbs did not alter cytokine/chemokine production by BMDCs nor BMDMs in vitro, with or without LPS stimulation (data not shown). With the highest concentration of bivalent Nb (40 $\mu\text{g}/\text{ml}$) we observed a small, but significant, increase in TNF production by DCs and TNF and IL1Ra production by macrophages in vitro. Importantly however, the highest in vivo dose of Nb used in this study (5 μg monovalent Nb+200 μg bivalent Nb) did not induce any significant increase in the serum cytokine levels, both for naive and tumor-bearing mice (FIG. 28). Overall, we conclude that anti-MMR Nbs are innovative tools for the targeting and imaging of hypoxic MMR⁺ TAMs without the risk of inducing overt innate immune responses in vivo.

Example 24

Relevance of MMR as a Marker for Tumor-Promoting Tams in Human Tumors

In order to test the relevancy of MMR as a marker for tumor-promoting TAMs in human tumors, we assessed MMR

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and CD68 (as human macrophage marker) expression in paraffin-embedded sections of human breast cancer samples (VUB-UZ Brussel). Using immunohistochemistry on consecutive slides of the same specimen and one double staining on a single slide, we could demonstrate the presence of CD68 positive macrophages in both tumor and fibrotic foci within the tumor region. Immunostaining for MMR clearly shows that the macrophages found in fibrotic foci do co-express MMR (data not shown). Since fibrotic foci within the tumor region is known to be a marker of hypoxia and worse prognosis,⁽⁴⁸⁾ the presence of MMR⁺ macrophages could function as an indicator of severe hypoxia in human tumors as well, similar to what we show for mouse tumors.

In summary, these studies shows that in human breast cancer samples, MMR⁺ TAMs are clearly detected and are enriched in fibrotic foci which are known to be a marker for intratumoral hypoxia and correlate with a poor prognosis.

Example 25

Selection of Anti-Human MMR Nbs

Next, anti-human MMR nanobodies were generated (see also Material and Method section). After four panning rounds of an anti human/anti mouse MMR phage bank on human MMR, up to 100-fold enrichments for hMMR reactive phages were observed per panning round. Therefore, 188 colonies from all rounds were selected for PE-expression. These PE-extracts were used in PE-ELISAs to determine which clones react effectively to hMMR. In total 100 clones were selected based on these results (FIG. 29). Additionally, the DNA and protein sequence of the selected clones was determined (Table 11) and double clones or premature stopping clones were discarded.

Example 26

Selection of Anti-Human/Mouse MMR Cross-Reactive Nbs

Next, anti-human/mouse MMR cross-reactive nanobodies were generated (see also Material and Method section). The anti human/anti mouse MMR phage bank was alternately screened on human and mouse MMR for a total of four rounds, resulting in up to 100-fold enrichments for hMMR/mMMR reactive phages from the second panning round. Therefore, 188 colonies from the second and third rounds were selected for PE-expression. These PE-extracts were used in PE-ELISAs to determine which clones react effectively to MMR, clones were selected after the ELISA on hMMR (FIG. 30). These clones were then screened for binding on mouse MMR (FIG. 31). Only clones⁽⁴²⁾ that reacted to both antigens were withheld as true cross-reactive Nbs. These clones were sequenced (Table 12) and divided into families based on their CDR3 regions.

Example 27

































Production of Representative Set of Anti-Human or Anti-Human/Mouse MMR Nbs

A set of representative clones was selected for Nb production in *E. Coli*: (1) anti-human Nbs: NbhMMRm1.33, NbhMMRm10.19, NbhMMRm23.30, NbhMMRm2.15, NbhMMRm3.1, NbhMMRm5.38, NbhMMRm12.6, NbhMMRm11.5, NbhMMRm15.43, NbhMMRm16.95; (2) anti-human/mouse Nbs: NbhmmMMRm14.4,

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


NbhmMMRm6.71, NbhmMMRm20.52, NbhmMMRm22.84, NbhmMMRm21.22, NbhmMMRm17.72, NbhmMMRm7.67, NbhmMMRm4.83 Each clone was grown in a two-liter culture. After expression and osmotic shock, the resulting extract was purified on 1 ml of Ni-NTA resin. The resulting 5 ml of eluted Nb was dialyzed to PBS after which the concentration was determined using a Nanodrop device and purity was assessed on Coomassie stained SDS-PAGE gels. The nanobodies all produced between 0.7 and 9 mg Nb/1 *E. coli* culture (Table 13).

TABLE 1

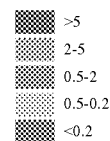
Gene expression profile of MHC II ^{hi} versus MHC II ^{low} TAMs						
Gene	GeneID	hi/low	hi/low	90% CI	p	ΔC_T hi
Ccl17	MGI: 1329039		30	[19-47]	**	8.1 ± 0.3
Cx3cl1	MGI: 1097153		9.2	[4.4-19]	*	12.2 ± 0.5
Cxcl11	MGI: 1860203		7.4	[4.2-13]	**	9.2 ± 0.1
Ccl5	MGI: 98262		6.1	[4.1-8.9]	*	5.4 ± 0.4
Il6	MGI: 96559		5.9	[1.8-19]		14 ± 0.9
Cxcl10	MGI: 1352450		5.9	[4.3-8.2]	*	5.4 ± 0.4
Cxcl9	MGI: 1352449		5.3	[4.2-6.6]	***	6.4 ± 0.0
Il12b	MGI: 96540		4.0	[1.6-10]		12.4 ± 0.4
Il1b	MGI: 96543		3.6	[2.6-5.1]	***	2.9 ± 0.1
Pgf	MGI: 105095		3.3	[0.68-16]		9.5 ± 0.5
Mmp9	MGI: 97011		2.9	[1.9-4.2]		4.0 ± 0.5
Ptgs2 (Cox2)	MGI: 97798		2.3	[1.1-5.0]		7.3 ± 0.6
Nos2 (iNOS)	MGI: 97361		2.3	[1.4-3.8]	*	8.8 ± 0.1
Angpt2	MGI: 1202890		2.1	[1.6-2.7]	**	9.2 ± 0.1
Ccl22	MGI: 1306779		2.0	[1.9-2.2]	*	11.5 ± 0.3
Tek (Tie2)	MGI: 98664		1.8	[1.5-2.2]		5.7 ± 0.4
Vegfa	MGI: 103178		1.6	[1.3-2.0]		6.2 ± 0.2
Thbs2 (TSP2)	MGI: 98738		1.2	[0.9-1.8]		13 ± 0.0
Il1a	MGI: 96542		1.2	[1.0-1.3]		6.8 ± 0.4
Il10	MGI: 96537		1.0	[0.69-1.5]		9.2 ± 0.3
Cxcl16	MGI: 1932682		0.97	[0.67-1.4]		4.1 ± 0.0
Tnf	MGI: 104798		0.93	[0.64-1.3]		5.1 ± 0.3
Thbs1 (TSP1)	MGI: 98737		0.89	[0.79-1.00]		6.2 ± 0.2
Cx3cr1	MGI: 1333815		0.85	[0.63-1.2]		7.4 ± 0.2
Mif	MGI: 96982		0.79	[0.67-0.93]		3.9 ± 0.1
Igfl	MGI: 96432		0.78	[0.63-0.97]		10.3 ± 0.4
Mmp14	MGI: 101900		0.77	[0.53-1.1]		8.3 ± 0.1
Ccr2	MGI: 106185		0.71	[0.39-1.3]		6.5 ± 0.5
Plau (uPA)	MGI: 97611		0.71	[0.62-0.81]		5.7 ± 0.1
Ccl11	MGI: 103576		0.7	[0.39-1.2]		12.6 ± 0.3
Adamts1	MGI: 109249		0.68	[0.44-1.0]		14.1 ± 0.3
Ccl1	MGI: 98258		0.65	[0.43-0.99]		12.5 ± 0.5
Tgfb1	MGI: 98725		0.64	[0.58-0.70]	*	4.5 ± 0.2
Cxcl1	MGI: 108068		0.64	[0.51-0.79]		3.5 ± 0.4

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TABLE 1-continued

Gene expression profile of MHC II ^{hi} versus MHC II ^{low} TAMs						
5	Ccl8	MGI: 101878		0.57	[0.33-0.98]	6.5 ± 0.4
	Il4ra	MGI: 105367		0.50	[0.44-0.57]	10.6 ± 0.2
	Arg1	MGI: 88070		0.48	[0.46-0.51]	** 1.7 ± 0.1
	Spp1	MGI: 98389		0.45	[0.40-0.51]	* 1.0 ± 0.1
	Ccl12	MGI: 108224		0.44	[0.30-0.64]	* 2.7 ± 0.2
10	Ccl6	MGI: 98263		0.39	[0.27-0.57]	* 1.9 ± 0.3
	Ccl4	MGI: 98261		0.34	[0.24-0.48]	** 4.8 ± 0.4
	Ctsd	MGI: 88562		0.33	[0.30-0.36]	** 4.4 ± 0.2
	Ccl9	MGI: 104533		0.33	[0.27-0.39]	** 2.5 ± 0.3
15	Ccl3	MGI: 98260		0.33	[0.25-0.43]	** 6.0 ± 0.2
	Timp2	MGI: 98753		0.30	[0.15-0.59]	* 4.8 ± 0.5
	Ccl2	MGI: 98259		0.26	[0.19-0.36]	* 2.7 ± 0.4
	Ccl7	MGI: 99512		0.25	[0.18-0.35]	** 2.9 ± 0.5
20	Mrc1 (MMR)	MGI: 97142		0.23	[0.21-0.25]	*** 4.2 ± 0.0
	Stab1	MGI: 2148742		0.22	[0.16-0.29]	** 5.5 ± 0.2
	CD163	MGI: 2135946		0.16	[0.12-0.21]	** 9.6 ± 0.1
	Lyve1	MGI: 2136348		0.033	[0.019-0.06]	* 8.5 ± 0.1

Protein	Gene	GeneID
Table 1 Legend		
30	FIG. 1	D7Rik132 (S12) MGI: 1338854
	CD11b	Itgam (Cd11b) MGI: 96607
	Ly6C	Ly6c1 (Ly6c) MGI: 96882
	Ly6G	Ly6g MGI: 109440
	CX ₃ CR1	Cx3cr1 MGI: 1333815
35	F4/80	Emr1 MGI: 106912
	CD62L	Sell (Cd62l) MGI: 98279
	CD49d	Itga4 (Cd49d) MGI: 96603
	CD162	Selp1g (Cd162) MGI: 106689
	CD11c	Itgax (Cd11c) MGI: 96609
	CD43	Spn (Cd43) MGI: 98384
40	SR-A	Msr1 MGI: 98257
	IL4-R α	Il4ra MGI: 105367
	CD80	Cd80 MGI: 101775
	CD86	Cd86 MGI: 101773
	PD-L1	Cd274 MGI: 1926446
45	PD-L2	Pdcd1lg2 MGI: 1930125
	FIG. 3	
	Arginase	Arg1 MGI: 88070
	FIG. 5	
50	CD4	Cd4 MGI: 88335
	CD8	Cd8a MGI: 88346



TAM subsets were sorted from 3 weeks tumor-bearing mice and their gene expression was assessed using qRT-PCR. The expression of each gene was normalized based on the S12 gene and is shown as the relative expression in MHC II^{hi} vs. MHC II^{low} TAMs (hi/low). Values are the geometric means of three to four independent experiments and are color-coded according to the level of induction. Accompanying 90% confidence intervals and p-values are shown.

*p < 0.05;

**p < 0.01;

***p < 0.001.

C_T represents the threshold cycle.

The ΔC_T was calculated for MHC II^{hi} TAMs and is defined as (C_T(gene) - C_T(S12)); values represent mean ± SEM. Lower ΔC_T corresponds to higher expression levels.

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TABLE 2

List of commercial antibodies		
Markers	Clone	Manufacturer
CD11b PE-Cy7	M1/70	BD Bioscience
Ly6C	ER-MP20	Serotec
AF647/AF488		
Ly6G PE/FITC	1A8	BD Bioscience
IA/IE PE/FITC	M5/114.15.2	BD Bioscience
IA/IE PercpCy5.5	M5/114.15.2	Serotec
IA/IE FITC	M5/114.15.2	eBioscience
F4/80 PE/FITC	CI:A3-1	Serotec
CCR3 FITC	83101	R&D Systems
CD62L PE	SK11	BD Bioscience
CD11c PE	HL3	BD Bioscience
CD43 PE	S7	BD Bioscience
CD49d PE	9C10(MFR4. B)	BD Bioscience

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TABLE 2-continued

List of commercial antibodies		
Markers	Clone	Manufacturer
CD162 PE	2PH1	BD Bioscience
MMR PE/FITC	MR5D3	Serotec
SR-A PE	2F8	Serotec
IL4R α	mIL4RM1	BD Bioscience
Tie-2 PE	TEK4	eBioscience
CD80 FITC	16-10A1	BD Bioscience
CD86 FITC	GL-1	BD Bioscience
PD-L1/PE	MIH5	eBioscience
PD-L2/PE	TY25	eBioscience
anti-TNF α /APC	MP6-XT22	BD Bioscience
Rabbit anti-iNOS	(M19)	Santa Cruz
anti-Rabbit/APC	polyclonal	Invitrogen

TABLE 3

List of gene specific primers		
GENE	FORWARD PRIMER	REVERSE PRIMER
CCL17	CCCATGAAGACCTTCACCTC (SEQ ID NO: 9)	CATCCCTGGAACACTCCACT (SEQ ID NO: 10)
CX3CL1	ACTCCTTGATTGGTGGGAAGC (SEQ ID NO: 11)	CAAAATGGCACAGACATTGG (SEQ ID NO: 12)
CXCL11	TCCTTTCCTCCAAATATCACG (SEQ ID NO: 13)	CAGCCATCCCTACCATTCTAT (SEQ ID NO: 14)
CCL5	GTGCCCACGTCAAGGAGTAT (SEQ ID NO: 15)	AGCAAGCAATGACAGGGAAG (SEQ ID NO: 16)
IL6	GTCTTCTGGAGTACCATAGC (SEQ ID NO: 17)	GTCAGATACCTGACAACAGG (SEQ ID NO: 18)
CXCL10	TCTGAGTCCCTCGCTCAAGTG (SEQ ID NO: 19)	CCTTGGAAGATGGTGGTTA (SEQ ID NO: 20)
CXCL9	TCAACAAAAGAGCTGCCAAA (SEQ ID NO: 21)	GCAGAGGCCAGAAGAGAGAA (SEQ ID NO: 22)
IL12B	GAAAGACCTTGACCATCACT (SEQ ID NO: 23)	CCTTCTCTGCAGACAGAGAC (SEQ ID NO: 24)
IL1B	GTGTGGATCCAAAGCAATAC (SEQ ID NO: 25)	GTCTGCTCATTCATGACAAG (SEQ ID NO: 26)
PGF	GCACTGTGTGCCGATAAAGA (SEQ ID NO: 27)	TACCTCCGGAAATGACATC (SEQ ID NO: 28)
MMP9	TGAATCAGCTGGCTTTTGTG (SEQ ID NO: 29)	GTGGATAGCTCGGTGGTGT (SEQ ID NO: 30)
PTGS2 (COX2)	CAGGCTGAACTTCGAAACAG (SEQ ID NO: 31)	CAGCTACGAAAACCAATCA (SEQ ID NO: 32)
NOS2	GCTTCTGGTCGATGTCATGAG (SEQ ID NO: 33)	TCCACCAGGAGATGTTGAAC (SEQ ID NO: 34)
ANGPT2	GCATGTGGTCCTTCCAATT (SEQ ID NO: 35)	GATCCTCAGCCACAACCTTC (SEQ ID NO: 36)
CCL22	TGACTTGGGTCTTGTCTCTC (SEQ ID NO: 37)	AAGGAAGCCACCAATGACAC (SEQ ID NO: 38)
TEK (TIE2)	ACTTCGAGGAGAACTGGAG (SEQ ID NO: 39)	AAGAAGCTGTTGGGAGGACA (SEQ ID NO: 40)
VEGFA	CAGGCTGCTGTAACGATGAA (SEQ ID NO: 41)	AATGCTTTCTCCGCTCTGAA (SEQ ID NO: 42)

TABLE 3-continued

List of gene specific primers		
GENE	FORWARD PRIMER	REVERSE PRIMER
THBS2 (TSP2)	GAAAGCATACCTGGCTGGAC (SEQ ID NO: 43)	ACAAAAGAGCCGTACCTGGA (SEQ ID NO: 44)
IL1A	TTTCAAAGGAAGGGGACAA (SEQ ID NO: 45)	CCACCTAGAAAACCTGCTG (SEQ ID NO: 46)
IL10	ACTCAATACACACTGCAGGTG (SEQ ID NO: 47)	GGACTTTAAGGGTTACTTGG (SEQ ID NO: 48)
CXCL16	GTCTCCTGCCTCCACTTTCT (SEQ ID NO: 49)	CTAAGGGCAGAGGGGCTATT (SEQ ID NO: 50)
TNF	CCTTCACAGAGCAATGACTC (SEQ ID NO: 51)	GTCTACTCCCAGGTTCTCTTC (SEQ ID NO: 52)
THBS1 (TSP1)	CGTTGCCATTGGAATAGAGA (SEQ ID NO: 53)	TGGCAAAGAGTCAAACCTGG (SEQ ID NO: 54)
CX3CR1	CACCATTAGTCTGGGCGTCT (SEQ ID NO: 55)	GATGCGGAAGTAGCAAAGC (SEQ ID NO: 56)
MIF	CTTTTAGCGGCACGAACGAT (SEQ ID NO: 57)	AAGAACAGCGGTGCAGGTAA (SEQ ID NO: 58)
IGF1	TGACATGCCCAAGACTCAGA (SEQ ID NO: 59)	AGGTTGCTCAAGCAGCAAAG (SEQ ID NO: 60)
MMP14	CCGGTACTACTGCTGCTCCT (SEQ ID NO: 61)	CACACACCGAGCTGTGAGAT (SEQ ID NO: 62)
CCR2	CTCAGTTCATCCACGCATA (SEQ ID NO: 63)	CAAGGCTCACCATCATCGTA (SEQ ID NO: 64)
PLAU (UPA)	TCTCCTGGCAAGGTAGGA (SEQ ID NO: 65)	GCCTGTGCAGAGTGAACAA (SEQ ID NO: 66)
CCL11	CTCCACAGCGCTTCTATTCC (SEQ ID NO: 67)	CTTCTTCTTGGGTCAGCAC (SEQ ID NO: 68)
ADAMTS1	CTGGGCAAGAAATCTGATGA (SEQ ID NO: 69)	TGGTTGTGGCAGGAAAGATA (SEQ ID NO: 70)
CCL1	GGATGTTGACAGCAAGAGCA (SEQ ID NO: 71)	CTCATCTTCACCCCGGTTAG (SEQ ID NO: 72)
TGFB1	CCAAGGAGACGGAATACAGG (SEQ ID NO: 73)	TCTCTGTGGAGCTGAAGCAA (SEQ ID NO: 74)
CXCL1	TCATAGCCCACTCAAGAATG (SEQ ID NO: 75)	AAGCAGAACTGAATACCATC (SEQ ID NO: 76)
CCL8	TCTACGAGTGTCTTTTGC (SEQ ID NO: 77)	CCACTTCTGTGTGGGTCTA (SEQ ID NO: 78)
IL4RA	GCAGATGGCTCATGTCTGAA (SEQ ID NO: 79)	CTCTGGGAAGCTGGGTGTAG (SEQ ID NO: 80)
ARG1	TCACCTGAGCTTTGATGTCG (SEQ ID NO: 81)	TTATGGTTACCTCCCGTTG (SEQ ID NO: 82)
SPP1	GCTTGGCTTATGGACTGAGG (SEQ ID NO: 83)	CTTGTCTTGTGGCTGTGAA (SEQ ID NO: 84)
CCL12	GCCTCCTGCTCATAGCTACC (SEQ ID NO: 85)	GGGTCAGCACAGATCTCCTT (SEQ ID NO: 86)
CCL6	ATGTCCAGCTTTGTGGGTTT (SEQ ID NO: 87)	AGGTCAGGTTCCGCAGATAA (SEQ ID NO: 88)
CCL4	CCCACTTCTGCTGTTTCTC (SEQ ID NO: 89)	GAGCAAGGACGCTTCTCAGT (SEQ ID NO: 90)
CTSD	CCTTCGCGATTATCAGAAATCC (SEQ ID NO: 91)	TACTTATGGTGGACCCAGCA (SEQ ID NO: 92)

TABLE 3-continued

List of gene specific primers		
GENE	FORWARD PRIMER	REVERSE PRIMER
Ccl9	CCAGATCACACATGCAACAG (SEQ ID NO: 93)	CTATAAAAATAAACACTTAGAGCCA (SEQ ID NO: 94)
Ccl3	CGGAAGATTCCACGCCAATTC (SEQ ID NO: 95)	GGTGAGGAACGTGTCCTGAAG (SEQ ID NO: 96)
Timp2	ATCGAACCAGAGTGAATG (SEQ ID NO: 97)	GCTAGAAACCCAGCATGAG (SEQ ID NO: 98)
Ccl2	CACTCACCTGCTGCTACTCATTACGGATTACAGAGAGGGAAAAATGG (SEQ ID NO: 99)	(SEQ ID NO: 100)
Ccl7	GACAAAGAAGGGCATGGAAG (SEQ ID NO: 101)	CATTCCTTAGCGTGACCAT (SEQ ID NO: 102)
Mrc1 (MMR)	GCAAATGGAGCCGTCTGTGC (SEQ ID NO: 103)	CTCGTGGATCTCCGTGACAC (SEQ ID NO: 104)
Stab1	ACGGGAACTGCTTGATGTC (SEQ ID NO: 105)	ACTCAGCGTCATGTTGTCCA (SEQ ID NO: 106)
CD163	GAGCATGAATGAAGTGTCG (SEQ ID NO: 107)	TGCTGAAGTTGTCGTACAC (SEQ ID NO: 108)
Lyve1	CTGGCTGTTTGCTACGTGAA (SEQ ID NO: 109)	CATGAACTTGCCTCGTGTG (SEQ ID NO: 110)

TABLE 4

Anti- mouse CD206 (MMR) nanobodies (anti-MMR nanobody clone 1 and 3): monovalent en bivalent constructs and nanobodies	
DNA seq + His tag (clone 1) SEQ ID NO: 1	CAGGTGCAGCTGCAGGAGTCTGGAGGAGGCTTGGTGCAGCCTGGGGGGTCT CTGAGACTCTCCTGTGCAGCCTCTGGAACATCTTCAGTATCAATGCCATCG GCTGGTACCGCCAGGCTCCAGGGAAGCAGCGCAGTTGGTCGCAACTATTA CTCTTAGTGGTAGCACAACTATGCAGACTCCGTGAAGGGCCGATTCTCCAT CTCCAGAGACAACGCCAAGAACACGGTGTATCTGCAAATGAACAGCCTGAA ACCTGAGGACACGGCCGTCTATTACTGTAATGCTAACACCTATAGCGACTCT GACGTTTATGGCTACTGGGGCCAGGGACCCAGGTCACCGTCTCCTCACACC ACCATCACCATCAC
DNA seq - His tag (clone 1) SEQ ID NO: 2	CAGGTGCAGCTGCAGGAGTCTGGAGGAGGCTTGGTGCAGCCTGGGGGGTCT CTGAGACTCTCCTGTGCAGCCTCTGGAACATCTTCAGTATCAATGCCATCG GCTGGTACCGCCAGGCTCCAGGGAAGCAGCGCAGTTGGTCGCAACTATTA CTCTTAGTGGTAGCACAACTATGCAGACTCCGTGAAGGGCCGATTCTCCAT CTCCAGAGACAACGCCAAGAACACGGTGTATCTGCAAATGAACAGCCTGAA ACCTGAGGACACGGCCGTCTATTACTGTAATGCTAACACCTATAGCGACTCT GACGTTTATGGCTACTGGGGCCAGGGACCCAGGTCACCGTCTCCTCA
Protein + His tag (clone 1) SEQ ID NO: 3	QVQLQESGGGLVQPGGSLRLSCAASGNIFSIINAIGWYRQAPGKQRELVAITLS GSTNYADSVKGRFSISRDNAKNTVYLQMNLSKPEDTAVYYCNANTYSDSDVY GYWGGGTQVTVSSHHHHH
Protein - His tag (clone 1) SEQ ID NO: 4	QVQLQESGGGLVQPGGSLRLSCAASGNIFSIINAIGWYRQAPGKQRELVAITLS GSTNYADSVKGRFSISRDNAKNTVYLQMNLSKPEDTAVYYCNANTYSDSDVY GYWGGGTQVTVSS
DNA seq + His tag (clone 3) SEQ ID NO: 5	CAGGTGCAGCTGCAGGAGTCTGGAGGAGGATTGGTGCAGGCTGGGGGCTCT CTGAGACTCTCCTGTGCAGCCTCTGGACGCACCTTCAGTAGAGATGCCATGG GCTGGTCCCGCCAGGCTCCAGGGAAGGAGCGTGAGTTTGTAGCAGGTATTA GCTGGAGTGGTGGTAGCACATACTATGCAGACTCCGTGAAGGGCCGATTCA CCATCTCCAGGACGGCGCCAAGAACAAGGTAATCTGCAAATGAACAGCC TGAAACCTGAGGACACGGCCGTTTATTACTGTGCAGCATCGTCGATTTATGG GAGTGCGGTAGTAGATGGGCTGTATGACTACTGGGGCCAGGGGACCCAGGT CACCGTCTCCTCACACCACCATCACATCAC

TABLE 4-continued

Anti- mouse CD206 (MMR) nanobodies (anti-MMR nanobody clone 1 and 3): monovalent en bivalent constructs and nanobodies	
DNA seq - His tag (clone 3) SEQ ID NO: 6	CAGGTGCAGCTGCAGGAGTCTGGAGGAGGATTGGTGCAGGCTGGGGGCTCT CTGAGACTCTCCTGTGCAGCCTCTGGACGCACCTTCAGTAGAGATGCCATGG GCTGGTTCCGCCAGGCTCCAGGGAAGGAGCGTGAGTTTGTAGCAGGTATTA GCTGGAGTGGTGGTAGCACATACTATGCAGACTCCGTGAAGGGCCGATTCA CCATCTCCAGGGACGGCGCCAGAACACGGTAAATCTGCAATGAACAGCC TGAAACCTGAGGACACGGCCGTTTATTACTGTGCAGCATCGTCGATTTATGG GAGTGGGTAGTAGATGGGCTGTATGACTACTGGGGCCAGGGGACCCAGGT CACCGTCTCCTCA
Protein + His tag (clone 3) SEQ ID NO: 7	QVQLQESGGGLVQAGGSLRLSCAASGRFTSRDAMGWFRQAPGKEREFVAGIS WSGGSTYYADSVKGRFTISRDAKNTVNLQMNSLKPEDTAVYYCAASSIYGSA VVDGLDYWGQGTQVTVSSHSHHHH
Protein - His tag (clone 3) SEQ ID NO: 8	QVQLQESGGGLVQAGGSLRLSCAASGRFTSRDAMGWFRQAPGKEREFVAGIS WSGGSTYYADSVKGRFTISRDAKNTVNLQMNSLKPEDTAVYYCAASSIYGSA VVDGLDYWGQGTQVTVSS
DNA seq + His tag (MMR biv IgA) SEQ ID NO: 111	CAGGTGCAGCTTCAGGAGTCTGGAGGAGGCTTGGTGCAGCCTGGGGGCTCT CTGAGACTCTCCTGTGCAGCCTCTGGAAACATCTTCAGTATCAATGCCATCG GCTGGTACCGCCAGGCTCCAGGGAAGCAGCGCGAGTTGGTCGCAACTATTA CTCTTAGTGGTAGCACAACTATGCAGACTCCGTGAAGGGCCGATTCTCCAT CTCCAGAGACAACGCCAAGAACACGGTGTATCTGCAATGAACAGCCTGAA ACCTGAGGACACGGCCGCTCTATTACTGTAATGCTAACACCTATAGCGACTCT GACGTTTATGGCTACTGGGGCCAGGGGACCCAGGTACCGTCTCCTCAAGC CCATCTACACCTCCACACCATCACCATCCACACCCAGGCAAGTCAGGTGC AGCTGCAGGAGTCTGGAGGAGGCTTGGTGCAGCCTGGGGGGTCTCTGAGAC TCTCCTGTGCAGCCTCTGGAACATCTTCAGTATCAATGCCATCGGCTGGTA CCGCCAGGCTCCAGGGAAGCAGCGCGAGTTGGTCGCAACTATTACTCTTAG TGGTAGCACAACTATGCAGACTCCGTGAAGGGCCGATTCTCCATCTCCAG AGACAACGCCAAGAACACGGTGTATCTGCAATGAACAGCCTGAAACCTGA GGACACGGCCGCTCTATTACTGTAATGCTAACACCTATAGCGACTCTGACGTT TATGGCTACTGGGGCCAGGGGACCCAGGTACCGTCTCCTCACACCACCATC ACCATCAC
Protein + His tag (MMR biv IgA) SEQ ID NO: 112	QVQLQESGGGLVQPGGSLRLSCAASGNIFSIINAIGWYRQAPGKQRELVATITLS GSTNYADSVKGRFSISRDAKNTVYLQMNSLKPEDTAVYYCNANTYSDSDVY GYWGQGTQVTVSSSPSTPPTPSPSTPPASQVQLQESGGGLVQPGGSLRLSCAAS GNIFSIINAIGWYRQAPGKQRELVATITLSGSTNYADSVKGRFSISRDAKNTVYL QMNSLKPEDTAVYYCNANTYSDSDVYGYWGQGTQVTVSSHSHHHH
DNA seq + His tag (MMR biv (Gly4Ser)3) SEQ ID NO: 113	CAGGTGCAGCTTCAGGAGTCTGGAGGAGGCTTGGTGCAGCCTGGGGGCTCT CTGAGACTCTCCTGTGCAGCCTCTGGAAACATCTTCAGTATCAATGCCATCG GCTGGTACCGCCAGGCTCCAGGGAAGCAGCGCGAGTTGGTCGCAACTATTA CTCTTAGTGGTAGCACAACTATGCAGACTCCGTGAAGGGCCGATTCTCCAT CTCCAGAGACAACGCCAAGAACACGGTGTATCTGCAATGAACAGCCTGAA ACCTGAGGACACGGCCGCTCTATTACTGTAATGCTAACACCTATAGCGACTCT GACGTTTATGGCTACTGGGGCCAGGGGACCCAGGTACCGTCTCCTCAGGC GGAGCCGCTAGTGGCGGAGGTGGATCTGGAGGCGCGGTAGTCAGGTGCA GCTGCAGGAGTCTGGAGGAGGCTTGGTGCAGCCTGGGGGTCTCTGAGACT CTCCTGTGCAGCCTCTGGAAACATCTTCAGTATCAATGCCATCGGCTGGTAC CGCCAGGCTCCAGGGAAGCAGCGCGAGTTGGTCGCAACTATTACTCTTAGT GGTAGCACAACTATGCAGACTCCGTGAAGGGCCGATTCTCCATCTCCAGA GACAACGCCAAGAACACGGTGTATCTGCAATGAACAGCCTGAAACCTGAG GACACGGCCGCTCTATTACTGTAATGCTAACACCTATAGCGACTCTGACGTTT ATGGCTACTGGGGCCAGGGGACCCAGGTACCGTCTCCTCACACCACCATC ACCATCAC
Protein + His tag (MMR biv (Gly4Ser)3) SEQ ID NO: 114	QVQLQESGGGLVQPGGSLRLSCAASGNIFSIINAIGWYRQAPGKQRELVATITLS GSTNYADSVKGRFSISRDAKNTVYLQMNSLKPEDTAVYYCNANTYSDSDVY GYWGQGTQVTVSSGGGGGGGGGGGGQVQLQESGGGLVQPGGSLRLSCAA SGNIFSIINAIGWYRQAPGKQRELVATITLSGSTNYADSVKGRFSISRDAKNTVYL QMNSLKPEDTAVYYCNANTYSDSDVYGYWGQGTQVTVSSHSHHHH
DNA seq + His tag (MMR biv g2c) SEQ ID NO: 115	CAGGTGCAGCTTCAGGAGTCTGGAGGAGGCTTGGTGCAGCCTGGGGGCTCT CTGAGACTCTCCTGTGCAGCCTCTGGAAACATCTTCAGTATCAATGCCATCG GCTGGTACCGCCAGGCTCCAGGGAAGCAGCGCGAGTTGGTCGCAACTATTA CTCTTAGTGGTAGCACAACTATGCAGACTCCGTGAAGGGCCGATTCTCCAT CTCCAGAGACAACGCCAAGAACACGGTGTATCTGCAATGAACAGCCTGAA ACCTGAGGACACGGCCGCTCTATTACTGTAATGCTAACACCTATAGCGACTCT GACGTTTATGGCTACTGGGGCCAGGGGACCCAGGTACCGTCTCCTCAGCG CACCACAGCGAAGACCCAGCTCCAAAGCTCCAAAGCTCCAATGGCACAG GTGCAAGCTGCAGGAGTCTGGAGGAGGCTTGGTGCAGCCTGGGGGTCTCTG AGACTCTCCTGTGCAGCCTCTGGAAACATCTTCAGTATCAATGCCATCGGCT

TABLE 4-continued

Anti- mouse CD206 (MMR) nanobodies (anti-MMR nanobody clone 1 and 3): monovalent en bivalent constructs and nanobodies	
	GGTACCGCCAGGCTCCAGGGAAGCAGCGCAGTTGGTCGCACTATTACTC TTAGTGGTAGCACAACTATGCAGACTCCGTGAAGGCCGATTCTCCATCTC CAGAGACAACGCCAAGAACACGGTGTATCTGCAATGAACAGCCTGAAACC TGAGGACACGGCCGTCTATTACTGTAATGCTAACACCTATAGCGACTCTGAC GTTTATGGCTACTGGGGCCAGGGGACCCAGGTCACCGTCTCCTCACACCACC ATCACCATCAC
Protein + His tag (MMR biv g2c) SEQ ID NO: 116	QVQLQESGGGLVQPGGSLRLSCAASGNIFSINAIGWYRQAPGKQRELVATITLS GSTNYADSVKGRFSISRDNAKNTVYLQMNLSLKPEDTAVYYCNANTYSDSDVY GYWGGQTQVTVSSAHHSEDPSSKAPKAPMAQVQLQESGGGLVQPGGSLRLSC AASGNIFSINAIGWYRQAPGKQRELVATITLSGSTNYADSVKGRFSISRDNAKNT VYLQMNLSLKPEDTAVYYCNANTYSDSDVYGYWGGQTQVTVSSHHHHH

TABLE 5

SPR kinetic and equilibrium parameters for anti-MMR Nanobodies and bivalent Nanobody 1 derivatives.						
Sample	k_a	SE (k_a)	k_d	SE (k_d)	K_D	Chi ²
Anti-MMR Nb1	5.76E+05	1.4E+3	0.01331	2.1E-5	2.31E-08	0.558
Anti-MMR Nb3	9.73E+04	1.6E+2	0.01859	2.2E-5	1.91E-07	0.190
biv MMR linker 1 GS	1.04E+06	4.9E+3	0.004404	1.4E-5	4.22E-09	3.56
biv MMR linker 2 g2c	1.02E+06	4.8E+3	0.004107	1.4E-5	4.04E-09	2.50
biv MMR linker 3 IgA	9.13E+05	1.5E+4	0.004285	5.3E-5	4.69E-09	2.25

Nb: Nanobody;
biv: bivalent;
GS: (Gly₄Ser)₃ linker;
g2c: llama IgG2 hinge linker;
IgA: human IgA hinge linker;
SE: standard error.

TABLE 6

Uptake values of ^{99m} Tc-labeled anti-MMR Nb clone 1 in naive and MMR ^{-/-} mice based on Pinhole SPECT/micro-CT at 1 hour post injection. Tracer uptake is expressed as percentage injected activity per gram cubic centimeter (% IA/cm ³).		
Organs/Tissues	MMR Nb in	
	WT (% IA/cm ³)	MMR Nb in MMR ^{-/-} (% IA/cm ³)
Heart	2.04 ± 0.21	1.13 ± 0.12
Lungs	5.96 ± 0.16	9.06 ± 2.43
Liver	18.66 ± 0.87	0.91 ± 0.16
Spleen	6.17 ± 0.31	0.34 ± 0.21
Kidney Left	80.98 ± 1.65	100.58 ± 0.4
Kidney Right	81.65 ± 2.32	102.82 ± 6.17
Muscle	1.74 ± 0.50	0.39 ± 0.22
Bone	5.02 ± 0.01	0.46 ± 0.02

TABLE 7

Uptake values of ^{99m} Tc-labeled bivalent anti-MMR Nb constructs (with (G ₄ S) ₃ , llama IgG2 hinge or human IgA hinge linkers), monovalent anti-MMR Nb clone 1, and control cAbBCIII10 Nb in naive and MMR ^{-/-} mice based on Pinhole SPECT/micro-CT at 1 hour post injection. Tracer uptake is expressed as percentage injected activity per gram cubic centimeter (% IA/cm ³).								
Organs-Tissues	(G4S) ₃ WT (% IA/cm ³)	(G4S) ₃ MMR ^{-/-} (% IA/cm ³)	Llama IgG2c WT (% IA/cm ³)	Llama IgG2c MMR ^{-/-} (% IA/cm ³)	Human IgA WT (% IA/cm ³)	Human IgA MMR ^{-/-} (% IA/cm ³)	MMR Nb WT (% IA/cm ³)	cAbBCIII10 WT (% IA/cm ³)
Heart	1.549 ± 0.057	0.541 ± 0.013	1.416 ± 0.147	0.440 ± 0.070	1.395 ± 0.083	0.505 ± 0.057	2.793 ± 0.043	0.693 ± 0.128
Lungs	1.053 ± 0.082	1.246 ± 0.038	0.987 ± 0.167	1.271 ± 0.130	0.936 ± 0.086	1.169 ± 0.161	2.543 ± 0.417	1.837 ± 0.271
Liver	20.857 ± 0.215	0.930 ± 0.081	20.491 ± 0.578	1.658 ± 0.077	21.571 ± 0.435	1.176 ± 0.044	13.670 ± 0.741	2.637 ± 0.203
Spleen	14.018 ± 1.669	0.634 ± 0.042	13.618 ± 1.497	1.347 ± 0.300	13.805 ± 1.353	0.477 ± 0.007	13.070 ± 0.251	0.933 ± 0.113
Kidney Left	26.381 ± 2.054	225.129 ± 13.936	24.257 ± 1.129	193.162 ± 8.114	26.728 ± 3.014	210.760 ± 14.414	160.443 ± 13.153	415.643 ± 15.162
Kidney Right	26.074 ± 2.227	212.682 ± 6.308	24.599 ± 2.053	202.343 ± 0.779	24.947 ± 2.463	214.144 ± 11.751	159.003 ± 13.700	408.597 ± 22.588
Muscle	0.251 ± 0.034	0.224 ± 0.010	0.158 ± 0.023	0.216 ± 0.015	0.212 ± 0.045	0.205 ± 0.004	ND	ND
Bone	1.466 ± 0.062	0.282 ± 0.016	1.041 ± 0.114	0.254 ± 0.030	1.089 ± 0.138	0.263 ± 0.022	ND	ND

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TABLE 8

Uptake values of ^{99m} Tc-labeled anti-MMR or cAbBCII10 Nb in TS/A tumor-bearing WT mice, based on dissection at 3 hours post injection. Tracer uptake is expressed as injected activity per gram tissue (% IA/g).		
Organs/Tissues	anti-MMR Nb in WT (% IA/g)	cAbBCII10 Nb in WT (% IA/g)
Heart	1.45 ± 0.12	0.10 ± 0.01
Lungs	1.55 ± 0.36	0.98 ± 0.12
Liver	12.60 ± 0.54	0.59 ± 0.02
Spleen	8.95 ± 0.60	0.24 ± 0.01
Kidney Left	79.67 ± 2.32	273.25 ± 14.76
Kidney Right	80.78 ± 3.62	261.16 ± 11.35
Muscle	0.52 ± 0.03	0.05 ± 0.01
Bone	1.33 ± 0.10	0.08 ± 0.01
Blood	0.13 ± 0.02	0.14 ± 0.01
Tumor	3.02 ± 0.10	0.40 ± 0.03

TABLE 9

Uptake values of ^{99m} Tc-labeled anti-MMR or cAbBCII10 Nb in 3LL tumor-bearing WT or MMR ^{-/-} mice, based on dissection at 3 hours post injection. Tracer uptake is expressed as injected activity per gram (% IA/g).			
Organs/Tissues	anti-MMR Nb in WT (% IA/g)	anti-MMR Nb in MMR ^{-/-} (% IA/g)	cAbBCII10 Nb in WT (% IA/g)
Heart	2.02 ± 0.11	0.06 ± 0.01	0.17 ± 0.01
Lungs	1.46 ± 0.05	1.02 ± 0.70	0.58 ± 0.04
Liver	9.55 ± 1.02	1.36 ± 1.06	1.03 ± 0.06
Spleen	4.61 ± 0.50	0.17 ± 0.02	0.41 ± 0.03
Kidney Left	108.61 ± 16.11	153.29 ± 27.22	368.79 ± 10.10
Kidney Right	88.60 ± 21.70	154.90 ± 20.71	305.21 ± 54.67

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TABLE 9-continued

Uptake values of ^{99m} Tc-labeled anti-MMR or cAbBCII10 Nb in 3LL tumor-bearing WT or MMR ^{-/-} mice, based on dissection at 3 hours post injection. Tracer uptake is expressed as injected activity per gram (% IA/g).			
Organs/Tissues	anti-MMR Nb in WT (% IA/g)	anti-MMR Nb in MMR ^{-/-} (% IA/g)	cAbBCII10 Nb in WT (% IA/g)
Muscle	0.61 ± 0.05	0.05 ± 0.02	0.08 ± 0.02
Bone	1.69 ± 0.10	0.06 ± 0.01	0.13 ± 0.01
Blood	0.10 ± 0.01	0.09 ± 0.01	0.24 ± 0.01
Tumor	3.02 ± 0.19	0.33 ± 0.03	0.74 ± 0.03

TABLE 10

Uptake values of ^{99m} Tc-labeled α-MMR Nb in s.c. 3LL-R tumor-bearing WT or CCR2-KO mice, based on dissection at 3 hours post injection. Tracer uptake is expressed as injected activity per gram (% IA/g).		
Organs/Tissues	α-MMR Nb in WT (% IA/g)	α-MMR Nb in CCR2-KO (% IA/g)
Heart	1.77 ± 0.06	1.94 ± 0.08
Lungs	1.54 ± 0.25	1.21 ± 0.10
Liver	14.1 ± 0.83	15.9 ± 0.65
Spleen	5.80 ± 0.25	7.14 ± 0.34
Kidney Left	103 ± 6.72	92.0 ± 7.56
Kidney Right	105 ± 7.55	92.7 ± 9.3
Muscle	0.36 ± 0.03	0.46 ± 0.06
Bone	1.04 ± 0.06	1.01 ± 0.03
Blood	0.16 ± 0.01	0.17 ± 0.01
Tumor	2.96 ± 0.22	1.81 ± 0.11

TABLE 11

Anti-human MMR Nbs selected after ELISA on human MMR of PE-extracts from single Nb clones isolated from phage display. In addition to the Nb sequence sensu strictu depicted here, all clones also carry a C-terminal extension containing a HA and 6xHis tag (AAAYPYDVPDYGSHHHHH; SEQ ID NO: 257).		
Name	SEQ ID NO:	Sequence

NbhMMR m1.33	126	QVQLQESGGGLVQPGGSLRLSCAASGFTLDNYIVANPQAPGKEREQVSC ISSSGSTNYADSVKGRFTISRDNKNSVTLQMNLSLEPDTAITYCAAEKAP FYTSVYFDDSTCVKASVDTWGQGTQVTVSS
NbhMMR m10.19	127	QVQLQESGGGLVQPGGSLRLSCAASGFTFSEIKTMGWYQAPGKQRELVAI TSGGSTNYADSVKGRFTISRDNKNTVYTLQMNLSLEPDTAVYYCNADSV VANLQGYHFWGQGTQVTVSS
NbhMMR m23.30	128	QVQLQESGGGLVQAGDSLSTSCAASGDTFNHYVSWGFQAPGKAREPVA AIFSGSGSKYADSVKGRPATSRDLAKNTVSLQMNLSLEPDTAVYYCAADR RFYMDWDDKSWVYWGQGTQVTVSS
NbhMMR m2.15	129	QVQLQESGGGLVQPGGSLRLSCASGFTLDYYDVGWFRQAPGKREPVSC EISCKHANYADSVKGRFTISRDNVKNITVYTLQMNLSLEPDTAITYCAAEKQ PYNEDGDTTRAEYVYWGQGTQVTVSS
NbhMMR m3.1	130	QVQLQESGGGLVQPGGSLRLSCAASGFTLDYYVVGWFRQAPGKREPVSC SYNCGSTTYADSVKGRFTISKDNKNTAYTLQMNLSLEPDTGITYCAAGSV CYNFWDTWGQGTQVTVSS
NbhMMR m5.38	131	QVQLQESGGGLVQAGGSLRLSCAASGFTDDYDVGWFRQAPGKEREQVSC ISSSGSTNYADSVKGRFTISRDNKNTVYTLQMNLSLEPDTAVYYCAADFF PNDGGSYVYVGRHATYDYGQGTQVTVSS
NbhMMR m12.6	132	QVQLQESGGGLVQPGGSLRLSCVVSGLSFLINMMGWYRQVSGEQRELVAI ITSGGSTNYADSVKGRFTISRDNKNTVYTLQMNLSLEPDTAVYYCHADAL TKLDPFFFWGQGTQVTVSS

TABLE 11-continued

Anti-human MMR Nbs selected after ELISA on human MMR of PE-extracts from single Nb clones isolated from phage display. In addition to the Nb sequence sensu strictu depicted here, all clones also carry a C-terminal extension containing a HA and 6xHis tag (AAAPYDVPDYGSHHHHH; SEQ ID NO: 257).		
Name	SEQ ID NO:	Sequence
NbhMMR m11.5	133	QVQLQESGGGLVQPGGSLRLSCAASGNIPTINRWGWRQAPGKQRELVA ATTSGGNTNYADSVKGRFTISRDNAKNTVYLQMNSLKPEDTAVYYCNARI VTMTSPYDDYWGQGTQVTVSS
NbhMMR m15.43	134	QVQLQESGGGLVQPGGSLRLSCAASGSTFSINRWGWRQAPGKQRELVA ITGGNTNYADSVKGRFTISRDNAKNTVYLQMNSLKPEDTAVYYCNANWG ATWGQGTQVTVSS
NbhMMR m16.95	135	QVQLQESGGGLVQPGGSLRLSCAASGRIASISAMGWWRQAPGKQRELVA ITGGNTNYADSVKGRFTISRDNAKNTVYLQMNSLKPEDTAVYYCNLLMV DYGLSLGDTYWGQGTQVTVSS
NbhMMR m4.83	136	QVQLQESGGGLVQPGGSLRLSCAASGPGFKLDYYAIWFRQAPGKEREGV SCIGSGGSLTYVENSVDKRFITSRDNAKNTVYLHMNSLKPEDTGIIYYCA ADTYYCSKPYWRIDYSGWGQGTQVTVSS

CDR1 (red), CDR2 (green) and CDR3 (blue) domains are also indicated, and are listed separately in Table 14.

TABLE 12

Anti-human/mouse MMR cross-reactive Nbs selected after ELISA on human MMR and mouse MMR of PE-extracts from single Nb clones isolated from phage display. In addition to the Nb sequence sensu strictu depicted here, all clones also carry a C-terminal extension containing a HA and 6xHis tag (AAAPYDVPDYGSHHHHH; SEQ ID NO: 257).

Name	SEQ ID NO:	Sequence
NbhmMM Rm14.4	137	QVQLQESGGGLVQAGDSRLRLSCAASGRTFSINRWGWRQAPGKQRELVA AITSGGNTNYADSVKGRFTISRDNAKNTVYLQMNSLKPEDTAVYYCNAD MDSLSCKGTYDANWGQGTQVTVSS
NbhmMM Rm6.71	138	QVQLQESGGGLVQAGGSLRLSCAASGGTFDDSVIGWFRQAPGKEREGVSC ISISGGNTNYADSVKGRFTISRDNAKNTVYLQMNSLKPEDTAVYYCAAREP EIGSGRTASVYDANWGQGTQVTVSS
NbhmMM Rm24.31	139	QVQLQESGGGLVQPGGSLRLSCTATGFTLKHHHIGWLRQAPGKEREGVAS INSGGNTNYADSVQGRFTISRDNAKNTVFLQMNSLKSEDTAVYYCAPLR RYENLNLQPSDYQWNGQGTQVTVSS
NbhmMM Rm20.52	140	QVQLQESGGGLVQAGGSLRLSCAASGRIPSAYAMGWFRQAPGKEREFVA AIGSGGNTDYADSVKGRFTISRDSAKNMVYLQMNSLKPEDTALYHCAAR TVSAPPDAWNGYWGQGTQVTVSS
NbhmMM Rm3.49	141	QVQLQESGGGLVQPGGSLRLSCAASGFSLDYYAIGWFRQAPGKEREGISCI SYKSGGNTNYADSVKGRFTISKDNAKNTAYLQMNSLKPEDTGIIYSCAAQV CYNDYWGQGTQVTVSS
NbhmMM Rm22.84	142	QVQLQESGGGLVQPGGSLRLSCAASGRTFSNYVNYAMGWFRQFP GKERE FVASISGSGNTTYADSVKGRFTISRDNAKNTVYLQMNSLKPEDTAVYYC AAALAQNTSDYATPDYHQPSAWGQGTQVTVSS
NbhmMM Rm19.52	143	QVQLQESGGGLVQAGGSLRLSCLASGDTFSNYVMRWFRQAPGKEREIVA AIGSGGNTDYADSVKGRFTISRDNAKNTAYLQMNSLKPEDTARYYCAAG KFWGQYAYWGQGTQVTVSS
NbhmMM Rm21.22	144	QVQLQESGGGLVQAGGSLRLSCAASGRTFSAAAMGWFRQAPGKEREPVA KIGGDDGNTTYADIAGRFTLSKDNAKNSVYLQMNSLKPEDTAVYYCAV KGRPDNNYENWGQGTQVTVSS
NbhmMM Rm14.93	145	QVQLQESGGGLVQAGDSRLRLSCAASGRTFSINRWGWRQAPGKQRELVA AITSGGNTNYADSVKGRFTISRDNAKNTVYLQMNSLKPEDTAVYYCNAD MDSLSGSGYVWGQGTQVTVSS

TABLE 12-continued

Anti-human/mouse MMR cross-reactive Nbs selected after ELISA on human MMR and mouse MMR of PE-extracts from single Nb clones isolated from phage display. In addition to the Nb sequence sensu strictu depicted here, all clones also carry a C-terminal extension containing a HA and 6xHis tag (AAAYPYDVPDYGSHHHHH; SEQ ID NO: 257).

Name	SEQ ID NO:	Sequence
NbhmMM Rm15.49	146	QVQLQESGGGLVQAGGSLRLSCAASGSTFSINNMGWYRQAPGKQRELVA GTGGGFTHYADSVKGRFTISRDNAKNTMYLQMNSLKPEDTAVYYCNATW GAWGQGTQVTSS
NbhmMM Rm17.72	147	QVQLQESGGGLVQPGGSLRLSCAASGSIVSINAMGWYRQAPGKQRELVA VTGGGRINLADSVKGRFTISRDNAKNTVYLQMNSLKPEDTAVYYCNVLV GFLGGYDVGQGTQVTSS
NbhmMM Rm10.79	148	QVQLQESGGGLVQPGGSLRLSCAASGSIFSIKTMGWYRQAPGKQRELVA VSSGGFTNYADSVKGRFTISRDNAKNAVYLMNSLKPEDTAVYYCNAGS VWAWGQPYDNTWGGQGTQVTSS

CDR1 (red), CDR2 (green) and CDR3 (blue) domains are also indicated, and are listed separately in Table 14.

TABLE 13

Production yields and physico-chemical characteristics of the anti-human MMR and anti-human/mouse MMR cross-reactive Nbs. All Nbs produce between 0.7 and 9 mg/l *E. coli* culture.

Name	number of A.A. Nb + HA + His	MW Nb + HA + His (dalton)	Theoretical pi	Extinction coefficient (assuming all Cys form cystines)	Estimated production capacity (g/l <i>E. Coli</i>)
anti-human MMR Nbs					
NbhMMRm1.33	152	16545	6.30	30620	0.7
NbhMMRm10.19	140	15188	6.63	31525	3.7
NbhMMRm23.30	144	16150	5.71	63035	2.3
NbhMMRm2.15	146	16095	5.58	29130	1.6
NbhMMRm3.1	137	14961	6.63	30620	1.1
NbhMMRm5.38	150	16535	5.51	36120	1.2
NbhMMRm12.6	138	15011	6.13	23045	1.7
NbhMMRm11.5	139	15106	7.17	26025	6.8
NbhMMRm15.43	131	14266	8.00	30035	6.2
NbhMMRm16.95	140	15025	7.17	26025	5.6
NbhMMRm4.83	149	16395	6.70	36120	3.0
anti-human/anti-mouse MMR Nbs					
NbhmMMRm14.4	141	15275	6.29	26025	1.6
NbhmMMRm6.71	144	15295	5.70	24660	2.4
NbhmMMRm24.31	144	15793	8.00	26025	1.0
NbhmMMRm20.52	143	15431	8.00	30035	5.4
NbhmMMRm3.49	137	14875	6.63	29130	1.6
NbhmMMRm22.84	149	16628	7.25	35995	4.2
NbhmMMRm19.52	136	14986	8.59	31525	4.1
NbhMMRm21.22	137	15045	5.91	26025	2.1
NbhmMMRm14.93	141	15289	6.63	26025	2.6
NbhmMMRm15.49	131	14226	8.00	30035	4.0
NbhmMMRm17.72	138	14896	7.18	24535	3.4
NbhmMMRm10.79	140	15130	6.63	31525	T.B.D
NbhmMMRm7.67	137	15153	7.18	30035	4.0
NbhmMMRm8.67	151	16635	6.76	40005	2.0
NbhmMMRm13.89	139	15096	6.70	30035	5.4
NbhmMMRm18.63	135	14393	7.18	34045	9.0
NbhmMMRm25.86	135	14891	6.29	24535	3.9
NbhmMMRm26.70	140	15299	7.18	24535	6.0
NbhmMMRm27.95	140	15392	7.22	24535	1.0

T.B.D.: to be determined

TABLE 14

CDRs of MMR-specific nanobodies				
Nanobody reference number	SEQ ID NO ¹	CDR1	CDR2	CDR3
Nanobody clone 1	4	SGNIFSINAIG (SEQ ID NO: 156)	TITLSGSTN (SEQ ID NO: 188)	NTYSDSDVYGY (SEQ ID NO: 220)
Nanobody clone 3	8	SGRTFSRDAMG (SEQ ID NO: 157)	GISWSGGST (SEQ ID NO: 189)	SSIYGS AVVDGLYD Y (SEQ ID NO: 221)
NbhMMRm1.33	126	GFTLDNYTVA (SEQ ID NO: 158)	CISSSGGST (SEQ ID NO: 190)	ERAPPYYS GYFFDS TCVAASYDY (SEQ ID NO: 222)
NbhMMRm10.19	127	GSIFSIKTMG (SEQ ID NO: 159)	AITSGGST (SEQ ID NO: 191)	DGVVAWDQPYDNY (SEQ ID NO: 223)
NbhMMRm23.30	128	GDTFNHYSWG (SEQ ID NO: 160)	AISWNGGS (SEQ ID NO: 192)	DRRPYNDWDDWS WWVY (SEQ ID NO: 224)
NbhMMRm2.15	129	GFTLDYYDIG (SEQ ID NO: 161)	CISSIGGSA (SEQ ID NO: 193)	EAQTPYNDGDCTRA SYDY (SEQ ID NO: 225)
NbhMMRm3.1	130	GFTLDYYAIG (SEQ ID NO: 162)	CISYKGGST (SEQ ID NO: 194)	GFVCYNYDY (SEQ ID NO: 226)
NbhMMRm5.38	131	GFTDDDDYDIG (SEQ ID NO: 163)	CISSSDGST (SEQ ID NO: 195)	DFFRWDSGSYYVRG CRHATYDY (SEQ ID NO: 227)
NbhMMRm12.6	132	GSFLSINHMG (SEQ ID NO: 164)	AITSGGST (SEQ ID NO: 196)	DALTMLPPPDF (SEQ ID NO: 228)
NbhMMRm11.5	133	GNIFTINRMG (SEQ ID NO: 165)	AITSGGNT (SEQ ID NO: 197)	AIVTMTSPYSYD (SEQ ID NO: 229)
NbhMMRm15.43	134	GSTFSINNMG (SEQ ID NO: 166)	GITGGNT (SEQ ID NO: 198)	NWGAY (SEQ ID NO: 230)
NbhMMRm16.95	135	GRIASISAMG (SEQ ID NO: 167)	AITGSGRT (SEQ ID NO: 199)	LMVDYGLGLGTDY (SEQ ID NO: 231)
NbhMMRm4.83	136	PGFKLDYYAIA (SEQ ID NO: 168)	CIGGSGSGLT (SEQ ID NO: 200)	DTYYYSKRVRWN DYGS (SEQ ID NO: 232)
NbhmmMRm14.4	137	GRTFSINYMG (SEQ ID NO: 169)	AITSGSGST (SEQ ID NO: 201)	DMDSSLGGYVDV (SEQ ID NO: 233)
NbhmmMRm6.71	138	GGTFDDSVIG (SEQ ID NO: 170)	CISSNDGTT (SEQ ID NO: 202)	ETPSIGSPTSASYD Y (SEQ ID NO: 234)
NbhmmMRm24.31	139	GFTLKNHHIG (SEQ ID NO: 171)	SINSSGGST (SEQ ID NO: 203)	LRRYYGLNLDPGSY DY (SEQ ID NO: 235)
NbhmmMRm20.52	140	GRIFSAYAMG (SEQ ID NO: 172)	AISRSGDST (SEQ ID NO: 204)	RTVSAPPSAAWGYG Y (SEQ ID NO: 236)
NbhmmMRm3.49	141	GFSLDYAIG (SEQ ID NO: 173)	CISYKGGST (SEQ ID NO: 205)	GFVCYNYDY (SEQ ID NO: 237)
NbhmmMRm22.84	142	GRTFSNYVNYAMG (SEQ ID NO: 174)	SISWSSVTT (SEQ ID NO: 206)	HLAQYSDYAYRDPH QFGA (SEQ ID NO: 238)
NbhmmMRm19.52	143	GDTFSNYVMA (SEQ ID NO: 175)	AIRLSGAR (SEQ ID NO: 207)	GHTWGQYAY (SEQ ID NO: 239)
NbhmmMRm21.22	144	GRTFSSAAMG (SEQ ID NO: 176)	LINLDDGET (SEQ ID NO: 208)	RGRFDDNYEY (SEQ ID NO: 240)

TABLE 14-continued

CDRs of MMR-specific nanobodies				
Nanobody reference number	SEQ ID NO ¹	CDR1	CDR2	CDR3
NbhmMMRm14.93	145	GRTFSINYMG (SEQ ID NO: 177)	AITSGSGST (SEQ ID NO: 209)	DMDSSLGGYVDV (SEQ ID NO: 241)
NbhmMMRm15.49	146	GSTFSINNMG (SEQ ID NO: 178)	GITGGNT (SEQ ID NO: 210)	NWGAY (SEQ ID NO: 242)
NbhmMMRm17.72	147	GSIVSINAMG (SEQ ID NO: 179)	LVTGSGRT (SEQ ID NO: 211)	LVIGPLEGYDY (SEQ ID NO: 243)
NbhmMMRm10.79	148	GSIFSITMG (SEQ ID NO: 180)	AVSSGGST (SEQ ID NO: 212)	DGVVAWDQPYDNY (SEQ ID NO: 244)
NbhmMMRm7.67	149	GRTFSVNAMA (SEQ ID NO: 181)	SITSSGLDT (SEQ ID NO: 213)	ERWDNGMVY (SEQ ID NO: 245)
NbhmMMRm8.67	150	GSMFSINAWG (SEQ ID NO: 182)	SITSGGGST (SEQ ID NO: 214)	ERWDGYALGYSPNH GSGHRPYNV (SEQ ID NO: 246)
NbhmMMRm13.89	151	GSIFSINAWG (SEQ ID NO: 183)	EITSSGST (SEQ ID NO: 215)	VAVTPTTPRSY (SEQ ID NO: 247)
NbhmMMRm18.63	152	GSIIISINAMA (SEQ ID NO: 184)	AISSGGST (SEQ ID NO: 216)	GGGWRPGA (SEQ ID NO: 248)
NbhmMMRm25.86	153	GFTVSTSMIN (SEQ ID NO: 185)	DVLPSGST (SEQ ID NO: 217)	NRETMPFF (SEQ ID NO: 249)
NbhmMMRm26.70	154	GFPFSAPMS (SEQ ID NO: 186)	YIGYTGIT (SEQ ID NO: 218)	GYARLIADSDLV (SEQ ID NO: 250)
NbhmMMRm27.95	155	GFPFNIYPMS (SEQ ID NO: 187)	YISHGTTT (SEQ ID NO: 219)	GYARLMTDSELV (SEQ ID NO: 251)

¹Nanobody sequences without His tag

TABLE 15

Amino acid sequences of human and mouse macrophage mannose receptor		
Name	SEQ ID NO	Amino acid sequence
Human MMR (MRC1)	258	MRLPLLVPASVIPGAVLLLDTRQFLIYNEDHKRCVDAVSPSAVQ TAACNQDAESQKFRWVSESIQMSVAFKLCGLVPSKTDWVAITLY ACDSKSEFQKWECKNDTLLGIKGEDLFFNYGNRQEKINIMLYKGS GLWSRWKIYGTDLNLCRSGYEAMYTLLGNANGATCAFPKFKENK WYADCTSAGRSDGWLWCGTTDDYDTDKLFGYCPLKFEGSESLW NKDPLTSVSYQINSKALTWHQARKSCQQNAELLSITEIHEQTYL TGLTSSLTSLGLWIGLNSLFSNGWQSDRSPFRYLNWLPGPSAE PGKSCVSLNPGKNAKWNLECVQKLGYICKKGNLTLSFVIPSSES DVPTHCPSQWWPYAGHCYKIHRDEKKIQDALTTCKREGDLTS IHTIEELDFIISQLGYEPNDELWIGLNDIKIQMYFEWSDGTPVTFTK WLRGEPSENNRQEDCVVMKGKDGWADRGEWPLGYICKMK SRSQGPEIVEVEKCRKGWKKHHFYCYMIGHTLSTFAEANQTCN NENAYLTITIEDRYEQAFLTSFVGLRPEKYFWTGLSDIQTGKTFQW TIEEEVRFTHWNNDMPGRKPGCVAMRTGIAGGLWDVLKCKDEKA KPVCKHWAEGVTHPPKPTTTPPKCPEDWGASSRTLSCFKLYAK GKHEKKTWFESRDFCRALGGDLASINNKEEQTIWRLITASGSYH KLFWLGLTYGSPSEGFTWSDGSPVSYENWAYGEPNNYQNV EYC GELKGDPTMSWNDINCEHLNNWICQIQKGQTPKPEPTAPQDNPP VTEDGWVIYKYQYFYSKEKETMDNARAFCKRNFGDLVSIQSES EKKFLWKYVNRNDAQSAYFIGLLISLDKKFAWMDGSKVDYVSW ATGEPNFANEDENCVTMYSNSGFWNIDINCGYPNAFICQRHNSIN ATTVMPTMPSPVSGCKEGWNFYSNKCFKIFGFMEEERKNWQEAR KACIGPGGNLVSIQNEKEQAFLYHMKDSTFSAWTGLNDVNSEH TFLWTDGRGVHYTNWKGYPGGRSSLSYEDADCVVIIGASNE AGKWMDDTCDSKRGYICQTRSDPSLTNPATIQTDGFVKYKSS YSLMRQKFQWHEAETCYCKLHNSLIASILDYPYSAFAWLQMETSN ERVWIALNSNLTNDNQYTWTDKWRVRYTNWAADPEPKLSACVY

TABLE 15-continued

Amino acid sequences of human and mouse macrophage mannose receptor		
Name	SEQ ID NO	Amino acid sequence
		LDLDGYWKTAKHCNESFYFLCKRSEIPATEPPQLPGRCPESDHTA WIPFHGHCHYIIESSYTRNWQASLECLRMGSSLSVIESAAESSFLS YRVEPLKSKTNFWIGLFRNVEGTWLVWNNSPVSVFNWNTGDPG ERNDCVALHASSGFWSNIHCSSYKGYICKRPKI IDAKPTHELLTTK ADTRKMDPSKPSNVAGVVIIVILLILTGAAGLAAYFFYKKRRVHLP QEGAFENTLYFNSQSSPGTSDMKDLVGNIEQNEHSVI
Recombinant human MMR (R&D systems)	259	LLDTRQFLIYNEDHKRCVDVSPSAVQTAACNQDAESQKFRWVS ESQIMSVAFKLC LGVPSKTDWVAITLYACDSKSEFQKWECKNDT LLGIKGEDLFFNYGNRQEKNIIMLYKSGLSRWKIYGTDTNLC RGYEAMYTLLGNANGATCAFPFKFENKWIADCTSAGRSDGWL WCGTTTDYD TKLFGYCPKFEGSESLWNKDPLTSVSYQINSKSA LTHWQARKSCQQQNAELLSITIEHQTYLTGLTSSLTSLGLWIGLNS LSFNSGWQSDRSPFRYLNWLPGPSAEPGKSCVSLNPGKNAKW ENLECVQKLGYICKKGNTLNSFVIPSESDVPTHCPQWWPYAGH CYKIHREDEKKIQRDALTCKRKEGDLASIHTEIEFDIIISQLGYEPN DELWIGLNDIKIQMYFEWSDGTPVTFKWLGRPEPSHENNRQEDC VVMKGKDGWADRGCWPLGYICKMKSRSQGPEIVEKEGCRK GWKKHHFYCYMIGHTLSTFAEANQTCNNENAYLTITIEDRYEQAF LTSFVGLRPEKYFWTGLSDIQTKGTFQWTEIEEVRFTHWNSDMPG RKPGCVAMRTGIAGGLWDLKCDKAKFVCKHWAEGVTHPPKP TTTPEPKCPEDWGASSRTSLCFKLYAKGKHEKKTWFESRDFCRAL GGDLASINNKEEQTIWRLITASGSYHKLFWLGLTYGSPSEGFTW SDGSPVSYENWAYGEPNNYQNVEYCGELKGDPTMSWNDINCEH LNNWICQIQKGQTPKPEPTPAPQDNPPVTEGWWIYKDYQYFYSK EKETMDNARAFCKRNFGLVSIQSESEKKFLWKYVNRNDASQAY FIGLLISLDKFAWMDGSKVDYVSWATGEPNFANEDENCVTMYS NSGFWNDCINCGYPNAFICQRHNSINATTVMPTMPSPVSGCKEGW NFYSNCKCFKIFGPMEEERKNWQEARACIGFGGNLVS IQNEKEQA FLTYHMKDSTFSAWTGLNDVNSEHTFLWTDGRGVHYTNWKGK YPGGRSSLSYEDADCVVIGGASNEAGKWMDDTCDSCRGYICQ TRSDPSLTNPPATIQTDGFVKYKSSYSLMRQKQWHEAETCYKL HNSLIASILDPSNAFAWLQMETSNERNVIALNSNLTDNQYTW DKWRVRYTNWAADEPKLSACVYLDLDGYWKTAKHCNESFYFL CKRSEIPATEPPQLPGRCPESDHTAWIPFHGHCHYIIESSYTRNW QASLECLRMGSSLSVIESAAESSFLSYRVEPLKSKTNFWIGLFRN EGTWLVWNNSPVSVFNWNTGDPGGERND CVALHASSGFWSNIHC SSYKGYICKRPKI IDAKPTHELLTTKADTRKMDPSKHHHHH
Mouse MMR (Mrc 1)	260	MRLLLLLAFISVIPSVQLLDARQFLIYNEDHKRCVDALSAISVQT ATCNPEAESQKFRWVSQSIMSVAFKLC LGVPSKTDWASVTLYA CDKSEYQKWECKNDTLFGIKGTLEYFNNGRQEKNI KLYKSG LWSRWKVYGTDDLC SRGYEAMYSLLGNANGAVCAFPFKFENK WYADCTSAGRSDGWLWCGTTTDYDKDKLFGFCPLHFEGERLW NKDPLTGILYQINSKALTWHQARASCKQQNADLLSVTEIHEQMY LTGLTSSLSSGLWIGLNSLSVRSWQWAGGSPFRYLNWLPGPS EPGKSCVSLNPGKNAKWENLECVQKLGYICKKGNTLNPFIIPSA SDVPTGCPNQWWPYAGHCYRIHREKKIKYALQACRKEGDL ASIHSEIEFDIFISQLGYEPNDELWIGLNDIKIQMYFEWSDGTPVTF TKWLPGEPHENNRQEDCVVMKGKDGWADRACEQPLGYICK MVSQSHAVVPEGADKGRKGWKRHGFYCYLIGSTLSTFTDANHT CTNEKAYLTITVEDRYEQAFLTSLVGLRPEKYFWTGLSDVQNKGT FRWTVDEQVQFTHWNADMPGRKAGCVAMKTGVAGGLWDVLS CEEKAKFVCKHWAEGVTRPPEPTTTPEPKCPENWGTTSKTSMCF KLYAKGKHEKKTWFESRDFCKAIGGELASIKSKDEQQVIWRLITS SGSYHELFWLGLTYGSPSEGFTWSDGSPVSYENWAYGEPNNYQN VEYCGELKGDPMGSWNDINCEHLNNWICQIQKGKTLPEPTPAPQ DNPPVTADGWVIYKDYQYFYSKEKETMDNARAFCKKNFGDLATI KSESEKKFLWKYINKNGGQSPYFIGMLISMDKKFIWMDGSKVDF VAWATGEPNFANDDENCVTMYTNSGFWDCINCGYPNFIQCRH NSSINATAMPTTPTTPGCKEGWHLYKNKCFKIFGFANEKKSW QDARQACKGLKGNLVS IENAEQAFVTYHMRDSTFNWNTGLNDI NAEHMPLWTAGQGVHYTNWKGYPGGRSSLSYEDADCVVIG GNSREAGTWMDTCDSKQGYICQQTQTDPSLPVSPTTTPKDGFT YGKSSYSMLKLLPWHAEATYCKDHTSLLASILDPSNAFAWMK MHPFNVP IWIALNSNLTNNEYTWTDWRVRYTNWGADEPKLS ACVYMDVDGYWRTSYCNESFYFLCKKSDEIPATEPPQLPGKCPES EQTAWIPFYGHCHYFESSFTRSWQASLECLRMGASLSVIEAAE SSFLSYRVEPLKSKTNFWIGMFRNVEGKWLWLDNVPVFNWKT GDPGGERND CVVLASSGLWNNIHCSSYKGFICKMPKIIDPVTHS SITTKADQRKMDPQPKGSSKAAGVTVVLLIVIGAGVAAFFYK KRHALHIPQEATFENTLYFNSNLSPGTSDDKLMGYIEQNEHAI

TABLE 15-continued

Amino acid sequences of human and mouse macrophage mannose receptor		
Name	SEQ ID NO	Amino acid sequence
Recombinant mouse MMR (R&D systems)	261	<p> LLDARQFLIYNEDHKRCVDALS AISVQTATCNPEAESQKFRWVSD SQIMSVAFKLC LGVPSKTDWASVTLYACDSKSEYQKWECKNDTL FGIKGTELYFNYGNRQEKNIKLYKGSGLWSRWKVYGTDDLC SR GYEAMYSLLGNANGAVCAFPFKFENKWIADCTSAGRSDGWLW CGTTTDDYDKLFGFCPLHFEGERLWNKDPLTGILYQINSKSAL TWHQARASCKQQNADLLSVTEIHEQMYLTGLTSSLSGLWIGLNS LSVRSQWQAGGSPFRYLNWLPGPSSEPGKSCVSLNPGKNAKW ENLECVQKLG YICKKGNTLNPFI IPSASDVPTGCPNQWWPYAGH CYRIHREKKIQKYALQACRKEGGDLAS IHSIEEFDIFISQLGYEPN DELWIGLNDIKIQMYFEWSDGTPVTFKWLPGEP SHENNRQEDCV VMKGDGYWADRACEQPLGYICKMVSQSHAVVPEGADKGRK GWKRHGFYCYLIGSTLSTFTDANHTCTNEKAYLTTVEDRYEQAF LTSLVGLRPEKYFWTGLSDVQNKGTFRWTVDEQVQPTHWNADM PGRKAGCVAMKTGVAGGLWDVLSCEEKAKFVCKHWAEGVTRP PEPTTTPPKCPENWGTTSTKSMCFKLYAKGHEKKTWFESRDFC KAIGGELASIKSKDEQQVIWRLITSSGSYHELFWLGLTYGSPSEGF TWSGSPVSYENWAYGEPNNYQNV EYCGELKGDPGMSWNDINC EHLNNWICQIQKGKTLLEPTPAPQDNPPVTADGWVIYKDYQYYF SKEKETMDNARAFCKKNFGDLATIKSESEKKFLWKYINKNGGQS PYFIGMLISMDKKFIWMDGSKVDFVAWATGEPNFANDDENCVT MYTNSGFWNDINCGYPNNFICQRHNS SINATAMPTTPTTPGGCKE GWHLKYKCKFKIFGFANEKKSWQDARQACKGLKGNLVS IENA QEQAFTVYHMRDSTFNAWTGLNDINAEHMF LWTAGQGVHYTN WGKGYPGRRSSLSYEDADCVV IIGGNSREAGTWMDTDCDSKQ GYICQTQTDPSLPVSPPTTPKDFV TYGKSSYSLMKLKL PWHEAE TYCKDHTSLLASILD PYSNAFAWMKMPFNVP IWIALNSNLTNNE YTWTDWRVRYTNWGADEPKLSACVYMDVDGYWRTSYCNES FYFLCKKSDEIPATEPPQLPGKCPSEQTAWIPFYGHCHYFESSFTR SWGQASLECLRMGASLVSIETAESSFLSYRVEPLKSKTNFWIGM FRNVEGKWLWLNPNVSVFNWKTGDP SGERND CVVLASSGLW NNHCSYKGFICKMPKIDPVTT HSSITTKADQRKMDPPQKGS SK AHHHHHH </p>
Human MMR (MRC1) - ectodomain	262	<p> LLDTRQFLIYNEDHKRCVD AVSPSAVQTAACNQDAESQKFRWVS ESQIMSVAFKLC LGVPSKTDWVAITLYACDSKSEFQKWECKNDT LLGIKGEDLFFNYGNRQEKNIKIMLYKGSGLWSRWKIYGTDDNLCS RGYEAMYTLLGNANGATCAFPFKFENKWIADCTSAGRSDGWL WCGTTTDDYDTDKLFGYCP LKFEGSESLWNKDPLTSVSYQINSKSA LTWHQARKSCQQNAELLSITEIHEQTYLTGLTSSLTSGLWIGLNS LSFNSGWQWSDRSPFRYLNWLPGPSAEPGKSCVSLNPGKNAKW ENLECVQKLG YICKKGNTLNSFVIPSESDVPTHCP SQWWPYAGH CYKIHRDEKKIQRDALTTCRKEGGDLTSIHTIEELDFIISQLGYEPN DELWIGLNDIKIQMYFEWSDGTPVTFKWL RGEPSHENNRQEDC VVMKGDGYWADRGC EWPLGYICKMKSRSQGPEIVEVEKGRK GWKKHHPYCYMIGHTLSTFAEANQTCNNENAYLTTVIEDRYEQAF LTSFVGLRPEKYFWTGLSDIQTKGTFQWTIEEEVRFTHWNSDMPG RKP GCVAMRTGIAGGLWDVLKDEKAKFVCKHWAEGVTHPPKP TTTPEPKCPEDWGASSRSLCFKLYAKGHEKKTWFESRDFCRAL GDLASINNKEEQQT IWRLITASGSYHKLFWLGLTYGSPSEGF TW SDGSPVSYENWAYGEPNNYQNV EYCGELKGDPTMSWNDINCEH LNNWICQIQKGQTPKPEPTPAPQDNPPVTEDGWVIYKDYQYYFSK EKETMDNARAFCKRNFGDLVSIQS ESEKKFLWKYVNRNDAQSAY FIGLLISLDKKFAWMDGSKVDYVSWATGEPNFANEDENCVTMYS NSGFWNDINCGYPNAFICQRHNS SINATVMPTMPSVP SGCKEGW NFYSNCKCFKIFGPMEEERKNWQ EARKACIGFGGNLVS IQNEKEQA FLTYHMKDSTFSAWTGLNDVNSEHTFLWTDGRGVHYTNWGKG YPGRRSSLSYEDADCVV IIGGASNEAGKWMDDTDCDSKRGYICQ TRSDPSLTNPPATIQTDGFKYKSSYSLMRQKFQWHEAET YCKL HNSLIASILD PYSNAFAWLQMETSNERNVIALNSNLTDNQYTW DKWRVRYTNWADEPKLSACVYLDLDGYWKT AHCNESFYFL CKRSDEIPATEPPQLPGRCPESDHTAWIPFYGHCHYI ESSYTRNWG QASLECLRMGSSLSVIESAAESSFLSYRVEPLKSKTNFWIGLFRNV EGTWLWINNSPVSVFNWNTGDP SGERND CVALHASSGFWSNIHC SSYKGYICKRPKIDAKP THELLTTKADTRKMDPSK </p>

TABLE 15-continued

Amino acid sequences of human and mouse macrophage mannose receptor		
Name	SEQ ID NO	Amino acid sequence
Mouse MMR (Mrc1) - ectodomain	263	LLDARQFLIYNEDHKRCVDALS AISVQTATCNPEAESQKFRWVSD SQIMSVAFKLC LGVP SKTDWASVTLYACDSKSEYQKWECKNDTL FGIKGTELYFNYGNRQEKNIKLYKSGSLWRKVKYGTDDLC SR GYEAMYSLLGNANGAVCAFPFKFENKWDYADCTAGRS DGLW CGTTTDDYDKDLFGFCPLHFEGERLWNKDPLTGILYQINSKSAL TWHQARASCQQNADLLSVTEIHEQMYLTGLTSSLSSGLWIGLNS LSVRS GQWAGGS PFYRLNWLPGSPSSEPGKSCVSLNPGKNAKW ENLECVQKLG YICKGNNTLNPFII PSASDVPTGCPNQWWPYAGH CYRIHREEKKIQKYALQACRKEGGDLAS IHSIEEFDFIFS QLYGEPN DELWIGLNDIKIQMYFEWSDGTPVTF TKWLPGEPSHENNRQEDCV VMKGKDG YWADRACEQPLGYICKMVSQSHAVVPEGADKGRK GWKRHGFYCYLIGSTLSTFTDANHTCTNEKAYLT TVEDRYEQAF L TSLVGLRPEKYPWTGLSDVQNKGTFRWTVDEQVQPTHWNADM PGRKAGCVAMKTGVAGGLWDVLSCEEKAKFVCKHWAEGVTRP PEPTTTPPKCPENWGTTSKTSMCKLYAKGKHEKKTWFESRDFC KAIGGELASIKSKDEQQVIWRLITSSGSYHELFWLGLTYGSPSEGF TWS DGS PVS YENWAYGEPNNYQNV EYCGELKGD PGM SWNDINC EHLNNWICQIQKGKTLLEPTPAPQDNPPVTADGWVIYKDYQYYF SKEKETMDNARAFCKKNFGDLATIKSESEKKFLWKYINKNGGQS PYFIGMLISMDKKFIWMDGSKVDFVAWATGEPNFANDDENCVT MYTNSGFWDINC GYPNNFICQRHNS SINATAMPTPTTPGGCKE GWHL YKNKCFKIFGFANEKKSWQDARQACKGLKGNLVS IENA QEQA FVTYHMRDSTFNAWTGLNDINA EHMFLW TAGQGVHYTN WGKGYPGGRSSLSYEDADCVVVI GGN SREAGTWMD DTCDSKQ GYICQTQTDPSLPVSP TTPKDFVTY GKS S YSLMKLKL PWHEAE TYCKDHTSLASILD PYSNAFAWMKMHFPNVPIWIALNSL TNNE YTWDRWRVRYTNWGADEPKLSACVYMDVDGYWR TSYCNES FYFLCKKSDEIPATEPPQLPGKCPSEQTAWIPFYGH CYYPFESSFTR SWGQASLECLRMGASLVS IETA AESSFLSYRVEPLKSKTNFWIGM FRNVEGKWLWLDNPNVSVFNWKTGDPSGERND CVVLASSGLW NNIHCSSYKGFICKMPKIIDPVTHSSITTKADQRKMDPQPKGSSK A

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35        40        45
Ala Thr Ile Thr Leu Ser Gly Ser Thr Asn Tyr Ala Asp Ser Val Lys
50        55        60
Gly Arg Phe Ser Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Tyr Leu
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Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys Asn
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 65 70 75 80
 Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys
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gtcttctgga gtaccatagc 20

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gtcagatacc tgacaacagg 20

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gcagaggcca gaagagagaa 20

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gcatgtggtc cttccaactt                20

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tgacttgggt ccttgcctc 20

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aaggaagcca ccaatgacac 20

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acttcgcagg agaactggag 20

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aagaagctgt tgggaggaca 20

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caggctgctg taacgatgaa 20

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aatgctttct ccgctctgaa 20

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acaaaagagc cgtacctgga 20

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tttcaaaagg aaggggacaa 20

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cgttgccatt ggaatagaga 20

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cacacaccga gctgtgagat

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caaggctcac catcatcgta

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<210> SEQ ID NO 65
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tctcctgggc aagtgtagga

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gcctgtgcag agtgaacaaa

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ctccacagcg cttctattcc

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cttcttcttg gggtcagcac

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tctacgcagt gcttctttgc 20

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ccacttctgt gtggggtcta 20

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gcagatggct catgtctgaa 20

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tcacctgagc tttgatgtcg 20

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<212> TYPE: DNA
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gagcaaggac gcttctcagt 20

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ctataaaaat aaacacttag agcca 25

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ggtgaggaac gtgtcctgaa g 21

<210> SEQ ID NO 97
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<212> TYPE: DNA
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atcgaaccca gagtggaatg 20

<210> SEQ ID NO 98
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<212> TYPE: DNA
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<400> SEQUENCE: 98

gctagaaacc ccagcatgag 20

<210> SEQ ID NO 99
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: artificial sequence
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<400> SEQUENCE: 99

cactcacctg ctgctactca ttcac 25

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gacaaagaag ggcattggaag 20

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gcaaatggag ccgtctgtgc 20

<210> SEQ ID NO 104
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<210> SEQ ID NO 105
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<210> SEQ ID NO 106
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<212> TYPE: DNA
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actcagcgtc atgttgtcca 20

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gagcatgaat gaagtgtccg 20

<210> SEQ ID NO 108
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<212> TYPE: DNA
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tgctgaagtt gtcgtcacac 20

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<212> TYPE: DNA
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catgaaactt gcctcgtgtg                                20

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<400> SEQUENCE: 111

cagggtgcagc ttcaggagtc tggaggaggc ttggtgcagc ctgggggggc tctgagactc    60
tctctgtgcag cctctggaaa catcttcagt atcaatgcc a tcggctggta ccgccaggct    120
ccagggaagc agcgcgagtt ggtcgcaact attactctta gtggtagcac aaactatgca    180
gactccgtga agggccgatt ctccatctcc agagacaacg ccaagaacac ggtgtatctg    240
caaatgaaca gcctgaaacc tgaggacacg gccgtctatt actgtaatgc taacacctat    300
agcgactctg acgtttatgg ctactggggc caggggaccc aggtcacctg ctctcaagc    360
ccatctacac ctcccacacc atcaccatcc acaccaccgg caagtcagggt gcagctgcag    420
gagtctggag gaggttgggt gcagcctggg gggctcttga gactctcttg tgcagcctct    480
ggaaacatct tcagtatcaa tgccatcggc tggtaaccgc aggtccagg gaagcagcgc    540
gagttggtcg caactattac tcttagtggt agcacaaact atgcagactc cgtgaagggc    600
cgattctcca tctccagaga caacgccaag aacacgggtg atctgcaa at gaacagcctg    660
aaacctgagg acacggccgt ctattactgt aatgctaaca cctatagcga ctctgacgtt    720
tatggctact ggggccaggg gacccaggtc accgtctcct cacaccacca tcaccatcac    780

<210> SEQ ID NO 112
<211> LENGTH: 260
<212> TYPE: PRT
<213> ORGANISM: Vicugna pacos

<400> SEQUENCE: 112

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1          5          10          15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Asn Ile Phe Ser Ile Asn
20        25        30

Ala Ile Gly Trp Tyr Arg Gln Ala Pro Gly Lys Gln Arg Glu Leu Val
35        40        45

Ala Thr Ile Thr Leu Ser Gly Ser Thr Asn Tyr Ala Asp Ser Val Lys
50        55        60

Gly Arg Phe Ser Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Tyr Leu
65        70        75        80

Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys Asn

```

[illegible]

caggtgcagc	ttcaggagtc	tggaggaggc	ttggtgcagc	ctggggggtc	tctgagactc	60
tctctgtcag	cctctggaag	catcttcagt	atcaatgcc	tgggctggta	ccgccaggct	120
ccagggaagc	agcgcgagtt	ggtcgcaact	attactctta	gtggtagcac	aaactatgca	180
gactccgtga	agggccgatt	ctccatctcc	agagacaacg	ccaagaacac	gggtgatctg	240
caaatgaaca	gcctgaaacc	tgaggacacg	gccgtctatt	actgtaatgc	taacacctat	300
agcgactctg	acgtttatgg	ctactggggc	cagggggacc	aggtcaccgt	ctctcagggc	360
ggaggcggta	gtggcggagg	tggatctgga	ggcggcggta	gtcaggtgca	gctgcaggag	420
tctggaggag	gcttggtgca	gcctgggggg	tctctgagac	tctcctgtgc	agcctctgga	480
aacatcttca	gtatcaatgc	catcggtctg	taccgccagg	ctccagggaa	gcagcgcgag	540
ttggtcgcaa	ctattactct	tagtggtagc	acaaactatg	cagactccgt	gaagggccga	600
ttctccatct	ccagagacaa	cgccaagaac	acggtgtatc	tgcaaatgaa	cagcctgaaa	660
cctgaggaca	cggccgtcta	ttaactgta	gctaacacct	atagcgactc	tgacgtttat	720
ggctactggg	gccaagggac	ccaaggtcac	gtctcctcac	accaccatca	ccatcac	777

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

-continued

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Asn Ile Phe Ser Ile Asn
 20 25 30
 Ala Ile Gly Trp Tyr Arg Gln Ala Pro Gly Lys Gln Arg Glu Leu Val
 35 40 45
 Ala Thr Ile Thr Leu Ser Gly Ser Thr Asn Tyr Ala Asp Ser Val Lys
 50 55 60
 Gly Arg Phe Ser Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Tyr Leu
 65 70 75 80
 Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys Asn
 85 90 95
 Ala Asn Thr Tyr Ser Asp Ser Asp Val Tyr Gly Tyr Trp Gly Gln Gly
 100 105 110
 Thr Gln Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
 115 120 125
 Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln Glu Ser Gly Gly Gly
 130 135 140
 Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly
 145 150 155 160
 Asn Ile Phe Ser Ile Asn Ala Ile Gly Trp Tyr Arg Gln Ala Pro Gly
 165 170 175
 Lys Gln Arg Glu Leu Val Ala Thr Ile Thr Leu Ser Gly Ser Thr Asn
 180 185 190
 Tyr Ala Asp Ser Val Lys Gly Arg Phe Ser Ile Ser Arg Asp Asn Ala
 195 200 205
 Lys Asn Thr Val Tyr Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr
 210 215 220
 Ala Val Tyr Tyr Cys Asn Ala Asn Thr Tyr Ser Asp Ser Asp Val Tyr
 225 230 235 240
 Gly Tyr Trp Gly Gln Gly Thr Gln Val Thr Val Ser Ser His His His
 245 250 255
 His His His

<210> SEQ ID NO 115

<211> LENGTH: 783

<212> TYPE: DNA

<213> ORGANISM: *Vicugna pacos*

<400> SEQUENCE: 115

cagggtgcagc ttcaggagtc tggaggaggc ttggtgcagc ctgggggggc tctgagactc 60
 tcctgtgcag cctctggaaa catcttcagt atcaatgcc a tcggctggta ccgccaggct 120
 ccagggaagc agcgcgagtt ggtcgcaact attactctta gtggtagcac aaactatgca 180
 gactccgtga agggccgatt ctccatctcc agagacaacg ccaagaacac ggtgtatctg 240
 caaatgaaca gcctgaaacc tgaggacacg gccgtctatt actgtaatgc taacacctat 300
 agcgactctg acgtttatgg ctactggggc cagggggacc aggtcaccgt ctctcagcg 360
 caccacagcg aagaccccag ctccaaagct cccaaagctc caatggcaca ggtgcagctg 420
 caggagtctg gaggaggctt ggtgcagcct ggggggtctc tgagactctc ctgtgcagcc 480
 tctggaaaca tcttcagtat caatgccatc ggctgggtacc gccaggctcc agggaagcag 540
 cgcgagttgg tcgcaactat tactcttagt ggtagcacia actatgcaga ctccgtgaag 600
 ggccgattct ccatctccag agacaacgcc aagaacacgg tgtatctgca aatgaacagc 660
 ctgaaacctg aggacacggc cgtctattac tgtaatgcta acacctatag cgactctgac 720

-continued

gtttatggct actggggcca ggggacccag gtcacgtct cctcacacca ccataccat 780
cac 783

<210> SEQ ID NO 116
<211> LENGTH: 261
<212> TYPE: PRT
<213> ORGANISM: Vicugna pacos

<400> SEQUENCE: 116

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Asn Ile Phe Ser Ile Asn
20 25 30
Ala Ile Gly Trp Tyr Arg Gln Ala Pro Gly Lys Gln Arg Glu Leu Val
35 40 45
Ala Thr Ile Thr Leu Ser Gly Ser Thr Asn Tyr Ala Asp Ser Val Lys
50 55 60
Gly Arg Phe Ser Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Tyr Leu
65 70 75 80
Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys Asn
85 90 95
Ala Asn Thr Tyr Ser Asp Ser Asp Val Tyr Gly Tyr Trp Gly Gln Gly
100 105 110
Thr Gln Val Thr Val Ser Ser Ala His His Ser Glu Asp Pro Ser Ser
115 120 125
Lys Ala Pro Lys Ala Pro Met Ala Gln Val Gln Leu Gln Glu Ser Gly
130 135 140
Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala
145 150 155 160
Ser Gly Asn Ile Phe Ser Ile Asn Ala Ile Gly Trp Tyr Arg Gln Ala
165 170 175
Pro Gly Lys Gln Arg Glu Leu Val Ala Thr Ile Thr Leu Ser Gly Ser
180 185 190
Thr Asn Tyr Ala Asp Ser Val Lys Gly Arg Phe Ser Ile Ser Arg Asp
195 200 205
Asn Ala Lys Asn Thr Val Tyr Leu Gln Met Asn Ser Leu Lys Pro Glu
210 215 220
Asp Thr Ala Val Tyr Tyr Cys Asn Ala Asn Thr Tyr Ser Asp Ser Asp
225 230 235 240
Val Tyr Gly Tyr Trp Gly Gln Gly Thr Gln Val Thr Val Ser Ser His
245 250 255
His His His His His
260

<210> SEQ ID NO 117
<211> LENGTH: 41
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 117

ccggccatgg cccaggtgca gcttcaggag tctggaggag g 41

<210> SEQ ID NO 118
<211> LENGTH: 88

-continued

```
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Primer
```

<400> SEQUENCE: 118

tgattcctgc agctgcacct gactaccgcc gcctccagat ccacctccgc cactaccgcc 60

tccgcctgag gagacggtga cctgggtc 88

```
<210> SEQ ID NO 119
<211> LENGTH: 94
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Primer
```

<400> SEQUENCE: 119

tgattctctgc agctgcacct gtgccattgg agctttggga gctttggagc tgggggtcttc 60

gctgtggtgc gctgaggaga cggtgacctg ggtc 94

```
<210> SEQ ID NO 120
<211> LENGTH: 91
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Primer
```

<400> SEQUENCE: 120

tgattcctgc agctgcacct gacttgccgg tgggtgtggat ggtgatggtg tgggaggtgt 60
agatgggctt gaggagacgg tgacctgggt c 91

```
<210> SEQ ID NO 121
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Linker
```

<400> SEQUENCE: 121

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1 5 10 15

```
<210> SEQ ID NO 122
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Linker
```

<400> SEQUENCE: 122

Ala His His Ser Glu Asp Pro Ser Ser Lys Ala Pro Lys Ala Pro Met
1 5 10 15

Ala

```
<210> SEQ ID NO 123
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Linker
```

<400> SEQUENCE: 123

Ser Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser Thr Pro Pro Ala Ser
1 5 10 15

-continued

<210> SEQ ID NO 124

<211> LENGTH: 40

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 124

attgaattct attagtgggtg gtggtgggtgg tgctcgagtg 40

<210> SEQ ID NO 125

<211> LENGTH: 33

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 125

ttaactgcag atggccgaag agggcggcag cct 33

<210> SEQ ID NO 126

<211> LENGTH: 133

<212> TYPE: PRT

<213> ORGANISM: Vicugna pacos

<400> SEQUENCE: 126

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu Asp Asn Tyr
20 25 30Thr Val Ala Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Gly Val
35 40 45Ser Cys Ile Ser Ser Ser Gly Gly Ser Thr Asn Tyr Ala Asp Ser Val
50 55 60Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Lys Ser Val Tyr
65 70 75 80Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Ile Tyr Thr Cys
85 90 95Ala Ala Glu Arg Ala Pro Pro Tyr Tyr Ser Gly Tyr Tyr Phe Phe Asp
100 105 110Ser Thr Cys Val Ala Ala Ser Tyr Asp Tyr Trp Gly Gln Gly Thr Gln
115 120 125Val Thr Val Ser Ser
130

<210> SEQ ID NO 127

<211> LENGTH: 121

<212> TYPE: PRT

<213> ORGANISM: Vicugna pacos

<400> SEQUENCE: 127

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Ser Ile Phe Ser Ile Lys
20 25 30Thr Met Gly Trp Tyr Arg Gln Ala Pro Gly Lys Gln Arg Glu Leu Val
35 40 45Ala Ala Ile Thr Ser Gly Gly Ser Thr Asn Tyr Ala Asp Ser Val Lys
50 55 60

-continued

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys Asn
85 90 95

Ala Asp Gly Val Val Ala Trp Asp Gln Pro Tyr Asp Asn Tyr Trp Gly
100 105 110

Gln Gly Thr Gln Val Thr Val Ser Ser
115 120

<210> SEQ ID NO 128
 <211> LENGTH: 125
 <212> TYPE: PRT
 <213> ORGANISM: *Vicugna pacos*

<400> SEQUENCE: 128

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Asp
1 5 10 15

Ser Leu Ser Ile Ser Cys Ala Ala Ser Gly Asp Thr Phe Asn His Tyr
20 25 30

Ser Trp Gly Trp Phe Arg Gln Ala Pro Gly Lys Ala Arg Glu Phe Val
35 40 45

Ala Ala Ile Ser Trp Asn Gly Gly Ser Lys Tyr Ala Asp Ser Val Lys
50 55 60

Gly Arg Phe Ala Ile Ser Arg Asp Ile Ala Lys Asn Thr Val Ser Leu
65 70 75 80

Gln Met Asn Ser Leu Glu Pro Glu Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Ala Asp Arg Arg Pro Tyr Asn Asp Trp Trp Asp Asp Trp Ser Trp Trp
100 105 110

Val Tyr Trp Gly Gln Gly Thr Gln Val Thr Val Ser Ser
115 120 125

<210> SEQ ID NO 129
 <211> LENGTH: 127
 <212> TYPE: PRT
 <213> ORGANISM: *Vicugna pacos*

<400> SEQUENCE: 129

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Glu
1 5 10 15

Ser Leu Arg Leu Ser Cys Lys Leu Ser Gly Phe Thr Leu Asp Tyr Tyr
20 25 30

Asp Ile Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Gly Val
35 40 45

Ser Cys Ile Ser Ser Ile Gly Gly Ser Ala Asn Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Val Lys Asn Thr Val Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Ile Tyr Tyr Cys
85 90 95

Ala Ala Glu Ala Gln Thr Pro Tyr Asn Asp Gly Asp Cys Thr Arg Ala
100 105 110

Ser Tyr Asp Tyr Trp Gly Gln Gly Ile Gln Val Thr Val Ser Ser
115 120 125

<210> SEQ ID NO 130

-continued

```

<211> LENGTH: 118
<212> TYPE: PRT
<213> ORGANISM: Vicugna pacos

<400> SEQUENCE: 130

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1          5          10          15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu Asp Tyr Tyr
20          25          30
Ala Ile Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Gly Ile
35          40          45
Ser Cys Ile Ser Tyr Lys Gly Gly Ser Thr Thr Tyr Ala Asp Ser Val
50          55          60
Lys Gly Arg Phe Thr Ile Ser Lys Asp Asn Ala Lys Asn Thr Ala Tyr
65          70          75          80
Leu Gln Met Asn Asn Leu Lys Pro Glu Asp Thr Gly Ile Tyr Tyr Cys
85          90          95
Ala Ala Gly Phe Val Cys Tyr Asn Tyr Asp Tyr Trp Gly Pro Gly Thr
100         105         110

Gln Val Thr Val Ser Ser
115

```

```

<210> SEQ ID NO 131
<211> LENGTH: 131
<212> TYPE: PRT
<213> ORGANISM: Vicugna pacos

<400> SEQUENCE: 131

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Gly
1          5          10          15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Asp Asp Asp Tyr
20          25          30
Asp Ile Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Gly Val
35          40          45
Ser Cys Ile Ser Ser Ser Asp Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50          55          60
Lys Gly Arg Phe Thr Ile Ser Ser Asp Asn Ala Lys Asn Thr Val Tyr
65          70          75          80
Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys
85          90          95
Ala Ala Asp Phe Phe Arg Trp Asp Ser Gly Ser Tyr Tyr Val Arg Gly
100         105         110
Cys Arg His Ala Thr Tyr Asp Tyr Trp Gly Gln Gly Thr Gln Val Thr
115         120         125

Val Ser Ser
130

```

```

<210> SEQ ID NO 132
<211> LENGTH: 119
<212> TYPE: PRT
<213> ORGANISM: Vicugna pacos

<400> SEQUENCE: 132

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1          5          10          15
Ser Leu Arg Leu Ser Cys Val Val Ser Gly Ser Phe Leu Ser Ile Asn
20          25          30

```


-continued

His Met Gly Trp Tyr Arg Gln Val Ser Gly Glu Gln Arg Glu Leu Val
 35 40 45

Ala Ala Ile Thr Ser Gly Gly Ser Thr Asn Tyr Ala Asp Ser Val Lys
 50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Ser Ala Lys Asn Thr Val Tyr Leu
 65 70 75 80

Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys Asn
 85 90 95

Ala Asp Ala Leu Thr Met Leu Pro Pro Phe Asp Phe Trp Gly Gln Gly
 100 105 110

Thr Gln Val Thr Val Ser Ser
 115

<210> SEQ ID NO 133
 <211> LENGTH: 120
 <212> TYPE: PRT
 <213> ORGANISM: *Vicugna pacos*

<400> SEQUENCE: 133

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Met Leu Ser Cys Ala Ala Ser Gly Asn Ile Phe Thr Ile Asn
 20 25 30

Arg Met Gly Trp Tyr Arg Gln Ala Pro Gly Lys Gln Arg Glu Leu Val
 35 40 45

Ala Ala Ile Thr Ser Gly Gly Asn Thr Asn Tyr Ala Asp Ser Val Lys
 50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Tyr Leu
 65 70 75 80

Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys Asn
 85 90 95

Ala Ala Ile Val Thr Met Thr Ser Pro Tyr Ser Asp Tyr Trp Gly Gln
 100 105 110

Gly Thr Gln Val Thr Val Ser Ser
 115 120

<210> SEQ ID NO 134
 <211> LENGTH: 112
 <212> TYPE: PRT
 <213> ORGANISM: *Vicugna pacos*

<400> SEQUENCE: 134

Gln Val Gln Leu Gln Glu Ser Gly Gly Thr Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Ser Thr Phe Ser Ile Asn
 20 25 30

Asn Met Gly Trp Tyr Arg Gln Ala Pro Gly Lys Gln Arg Glu Leu Val
 35 40 45

Ala Gly Ile Thr Gly Gly Asn Thr His Tyr Ala Asp Ser Val Lys Gly
 50 55 60

Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Met Tyr Leu Gln
 65 70 75 80

Met Asn Gly Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys Asn Ala
 85 90 95

Asn Trp Gly Ala Tyr Trp Gly Gln Gly Thr Gln Val Thr Val Ser Ser
 100 105 110

-continued

<210> SEQ ID NO 135
 <211> LENGTH: 121
 <212> TYPE: PRT
 <213> ORGANISM: *Vicugna pacos*

<400> SEQUENCE: 135

```

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1          5          10          15
Ser Leu Gly Leu Ser Cys Ala Ala Ser Gly Arg Ile Ala Ser Ile Ser
20          25          30
Ala Met Gly Trp Tyr Arg Gln Ala Pro Gly Lys Gln Arg Glu Leu Val
35          40          45
Ala Ala Ile Thr Gly Ser Gly Arg Thr Asn Tyr Ala Asp Ser Val Lys
50          55          60
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Tyr Leu
65          70          75          80
Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys Asn
85          90          95
Leu Leu Met Val Asp Tyr Gly Leu Gly Leu Gly Thr Asp Tyr Trp Gly
100         105         110
Gln Gly Thr Gln Val Thr Val Ser Ser
115         120

```

<210> SEQ ID NO 136
 <211> LENGTH: 130
 <212> TYPE: PRT
 <213> ORGANISM: *Vicugna pacos*

<400> SEQUENCE: 136

```

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1          5          10          15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Pro Gly Phe Lys Leu Asp
20          25          30
Tyr Tyr Ala Ile Ala Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu
35          40          45
Gly Val Ser Cys Ile Gly Gly Ser Gly Ser Gly Leu Thr Thr Tyr Val
50          55          60
Glu Asn Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asn Ala Gln
65          70          75          80
Asn Thr Val Tyr Leu His Met Asn Ser Leu Lys Pro Glu Asp Thr Gly
85          90          95
Ile Tyr Tyr Cys Ala Ala Asp Thr Tyr Tyr Tyr Cys Ser Lys Arg Val
100         105         110
Trp Arg Asn Asp Tyr Gly Ser Trp Gly Gln Gly Thr Gln Val Thr Val
115         120         125
Ser Ser
130

```

<210> SEQ ID NO 137
 <211> LENGTH: 122
 <212> TYPE: PRT
 <213> ORGANISM: *Vicugna pacos*

<400> SEQUENCE: 137

```

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Asp
1          5          10          15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Arg Thr Phe Ser Ile Asn

```

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20					25					30					
Tyr	Met	Gly	Trp	Tyr	Arg	Gln	Ala	Pro	Gly	Lys	Gln	Arg	Glu	Leu	Val
	35					40					45				
Ala	Ala	Ile	Thr	Ser	Gly	Ser	Gly	Ser	Thr	Asn	Tyr	Ala	Asp	Ser	Val
	50					55					60				
Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ala	Lys	Asn	Thr	Met	Tyr
	65					70					75				80
Leu	Gln	Met	Asn	Ser	Leu	Lys	Pro	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys
			85						90					95	
Asn	Ala	Asp	Met	Asp	Ser	Ser	Leu	Ser	Gly	Gly	Tyr	Val	Asp	Val	Trp
			100					105					110		
Gly	Gln	Gly	Thr	Gln	Val	Thr	Val	Ser	Ser						
	115					120									

<210> SEQ ID NO 138

<211> LENGTH: 125

<212> TYPE: PRT

<213> ORGANISM: Vicugna pacos

<400> SEQUENCE: 138

Gln	Val	Gln	Leu	Gln	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Ala	Gly	Gly
1			5					10						15	
Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Gly	Thr	Phe	Asp	Asp	Ser
		20						25				30			
Val	Ile	Gly	Trp	Phe	Arg	Gln	Ala	Pro	Gly	Lys	Glu	Arg	Glu	Gly	Val
		35				40						45			
Ser	Cys	Ile	Ser	Ser	Asn	Asp	Gly	Thr	Thr	His	Tyr	Ala	Ser	Pro	Val
	50				55					60					
Lys	Gly	Arg	Phe	Thr	Ile	Ser	Ser	Asp	Asn	Ala	Lys	Asn	Thr	Val	Tyr
	65				70				75					80	
Leu	Gln	Met	Asn	Ser	Leu	Lys	Pro	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys
			85					90						95	
Ala	Ala	Glu	Thr	Pro	Ser	Ile	Gly	Ser	Pro	Cys	Thr	Ser	Ala	Ser	Tyr
		100					105						110		
Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Gln	Val	Thr	Val	Ser	Ser			
		115					120					125			

<210> SEQ ID NO 139

<211> LENGTH: 125

<212> TYPE: PRT

<213> ORGANISM: Vicugna pacos

<400> SEQUENCE: 139

Gln	Val	Gln	Leu	Gln	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	Gly
1			5					10						15	
Ser	Leu	Arg	Leu	Ser	Cys	Thr	Ala	Thr	Gly	Phe	Thr	Leu	Lys	Asn	His
		20						25				30			
His	Ile	Gly	Trp	Leu	Arg	Gln	Ala	Pro	Gly	Lys	Glu	Arg	Glu	Gly	Val
		35				40						45			
Ala	Ser	Ile	Asn	Ser	Ser	Gly	Gly	Ser	Thr	Asn	Tyr	Ala	Asp	Ser	Val
	50					55					60				
Gln	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ala	Lys	Asn	Thr	Val	Phe
	65				70				75					80	
Leu	Gln	Met	Asn	Ser	Leu	Lys	Ser	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys
			85					90						95	
Ala	Arg	Leu	Arg	Arg	Tyr	Tyr	Gly	Leu	Asn	Leu	Asp	Pro	Gly	Ser	Tyr

-continued

100	105	110
Asp Tyr Trp Gly Gln Gly Thr Gln Val Thr Val Ser Ser		
115	120	125
<210> SEQ ID NO 140		
<211> LENGTH: 124		
<212> TYPE: PRT		
<213> ORGANISM: Vicugna pacos		
<400> SEQUENCE: 140		
Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Gly		
1	5	10 15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Arg Ile Phe Ser Ala Tyr		
20	25	30
Ala Met Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Phe Val		
35	40	45
Ala Ala Ile Ser Arg Ser Gly Asp Ser Thr Asp Tyr Ala Asp Ser Val		
50	55	60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Ser Ala Lys Asn Met Val Tyr		
65	70	75 80
Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Leu Tyr His Cys		
85	90	95
Ala Ala Arg Thr Val Ser Ala Pro Pro Ser Ala Ala Trp Gly Tyr Gly		
100	105	110
Tyr Trp Gly Gln Gly Thr Gln Val Thr Val Ser Ser		
115	120	

<210> SEQ ID NO 141
 <211> LENGTH: 118
 <212> TYPE: PRT
 <213> ORGANISM: Vicugna pacos

<400> SEQUENCE: 141

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly		
1	5	10 15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Leu Asp Tyr Tyr		
20	25	30
Ala Ile Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Gly Ile		
35	40	45
Ser Cys Ile Ser Tyr Lys Gly Gly Ser Thr Thr Tyr Ala Asp Ser Val		
50	55	60
Lys Gly Arg Phe Thr Ile Ser Lys Asp Asn Ala Lys Asn Thr Ala Tyr		
65	70	75 80
Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Gly Ile Tyr Ser Cys		
85	90	95
Ala Ala Gly Phe Val Cys Tyr Asn Tyr Asp Tyr Trp Gly Gln Gly Thr		
100	105	110
Gln Val Thr Val Ser Ser		
115		

<210> SEQ ID NO 142
 <211> LENGTH: 130
 <212> TYPE: PRT
 <213> ORGANISM: Vicugna pacos

<400> SEQUENCE: 142

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly		
1	5	10 15

-continued

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Arg Thr Phe Ser Asn Tyr
 20 25 30
 Val Asn Tyr Ala Met Gly Trp Phe Arg Gln Phe Pro Gly Lys Glu Arg
 35 40 45
 Glu Phe Val Ala Ser Ile Ser Trp Ser Ser Val Thr Thr Tyr Tyr Ala
 50 55 60
 Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn
 65 70 75 80
 Thr Val Tyr Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val
 85 90 95
 Tyr Tyr Cys Ala Ala His Leu Ala Gln Tyr Ser Asp Tyr Ala Tyr Arg
 100 105 110
 Asp Pro His Gln Phe Gly Ala Trp Gly Gln Gly Thr Gln Val Thr Val
 115 120 125
 Ser Ser
 130

<210> SEQ ID NO 143
 <211> LENGTH: 117
 <212> TYPE: PRT
 <213> ORGANISM: Vicugna pacos

<400> SEQUENCE: 143

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Gly
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Leu Ala Ser Gly Asp Thr Phe Ser Asn Tyr
 20 25 30
 Val Met Ala Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Ile Val
 35 40 45
 Ala Ala Ile Arg Leu Ser Gly Ala Arg Tyr Val Pro Asp Ser Val Lys
 50 55 60
 Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ala Met Tyr Leu
 65 70 75 80
 Gln Met Thr Ser Leu Lys Pro Glu Asp Thr Ala Arg Tyr Tyr Cys Ala
 85 90 95
 Ala Gly His Thr Trp Gly Gln Tyr Ala Tyr Trp Gly Gln Gly Thr Gln
 100 105 110
 Val Thr Val Ser Ser
 115

<210> SEQ ID NO 144
 <211> LENGTH: 119
 <212> TYPE: PRT
 <213> ORGANISM: Vicugna pacos

<400> SEQUENCE: 144

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Gly
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Arg Thr Phe Ser Ser Ala
 20 25 30
 Ala Met Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Pro Val
 35 40 45
 Ala Leu Ile Asn Leu Asp Asp Gly Glu Thr Tyr Tyr Ala Asp Ile Ala
 50 55 60
 Lys Gly Arg Phe Thr Leu Ser Lys Asp Asn Ala Lys Asn Ser Val Tyr
 65 70 75 80

-continued

Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Val Arg Gly Arg Phe Asp Asp Asn Tyr Glu Tyr Trp Gly Gln Gly
100 105 110

Thr Gln Val Thr Val Ser Ser
115

<210> SEQ ID NO 145

<211> LENGTH: 122

<212> TYPE: PRT

<213> ORGANISM: *Vicugna pacos*

<400> SEQUENCE: 145

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Asp
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Arg Thr Phe Ser Ile Asn
20 25 30

Tyr Met Gly Trp Tyr Arg Gln Ala Pro Gly Lys Gln Arg Glu Leu Val
35 40 45

Ala Ala Ile Thr Ser Gly Ser Gly Ser Thr Asn Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Lys Thr Met Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Asn Ala Asp Met Asp Ser Ser Leu Ser Gly Gly Tyr Val Asp Val Trp
100 105 110

Gly Gln Gly Thr Gln Val Thr Val Ser Ser
115 120

<210> SEQ ID NO 146

<211> LENGTH: 112

<212> TYPE: PRT

<213> ORGANISM: *Vicugna pacos*

<400> SEQUENCE: 146

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Ser Thr Phe Ser Ile Asn
20 25 30

Asn Met Gly Trp Tyr Arg Gln Ala Pro Gly Lys Gln Arg Glu Leu Val
35 40 45

Ala Gly Ile Thr Gly Gly Asn Thr His Tyr Ala Asp Ser Val Lys Gly
50 55 60

Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Met Tyr Leu Gln
65 70 75 80

Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys Asn Ala
85 90 95

Asn Trp Gly Ala Tyr Trp Gly Gln Gly Thr Gln Val Thr Val Ser Ser
100 105 110

<210> SEQ ID NO 147

<211> LENGTH: 119

<212> TYPE: PRT

<213> ORGANISM: *Vicugna pacos*

<400> SEQUENCE: 147

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Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Ser Ile Val Ser Ile Asn
 20 25 30
 Ala Met Gly Trp Tyr Arg Gln Ala Pro Gly Lys Gln Arg Glu Leu Val
 35 40 45
 Ala Leu Val Thr Gly Ser Gly Arg Thr Asn Leu Ala Asp Ser Val Lys
 50 55 60
 Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Tyr Leu
 65 70 75 80
 Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys Asn
 85 90 95
 Val Leu Val Ile Gly Pro Leu Glu Gly Tyr Asp Tyr Trp Gly Gln Gly
 100 105 110
 Thr Gln Val Thr Val Ser Ser
 115

<210> SEQ ID NO 148
 <211> LENGTH: 121
 <212> TYPE: PRT
 <213> ORGANISM: *Vicugna pacos*

<400> SEQUENCE: 148

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15
 Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Ser Ile Phe Ser Ile Lys
 20 25 30
 Thr Met Gly Trp Tyr Arg Gln Ala Pro Gly Lys Gln Arg Glu Leu Val
 35 40 45
 Ala Ala Val Ser Ser Gly Gly Ser Thr Asn Tyr Ala Asp Ser Val Lys
 50 55 60
 Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ala Val Tyr Leu
 65 70 75 80
 Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys Asn
 85 90 95
 Ala Asp Gly Val Val Ala Trp Asp Gln Pro Tyr Asp Asn Tyr Trp Gly
 100 105 110
 Gln Gly Thr Gln Val Thr Val Ser Ser
 115 120

<210> SEQ ID NO 149
 <211> LENGTH: 118
 <212> TYPE: PRT
 <213> ORGANISM: *Vicugna pacos*

<400> SEQUENCE: 149

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Gly
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Val Asp Gln Gly Arg Thr Phe Ser Val Asn
 20 25 30
 Ala Met Ala Trp Tyr Arg Gln Ala Pro Gly Lys Gln Arg Glu Leu Val
 35 40 45
 Ala Ser Ile Thr Ser Ser Gly Leu Asp Thr Gln Tyr Ala Glu Gly Met
 50 55 60
 Lys Gly Arg Phe Thr Ile Ser Lys Gly Asn Asp Lys Phe Ser Thr Tyr
 65 70 75 80

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Leu Gln Met Asn Asn Leu Lys Pro Asp Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Asn Ala Glu Arg Trp Asp Asn Gly Met Val Tyr Trp Gly Lys Gly Thr
 100 105 110

Gln Val Thr Val Ser Ser
 115

<210> SEQ ID NO 150
 <211> LENGTH: 132
 <212> TYPE: PRT
 <213> ORGANISM: *Vicugna pacos*

<400> SEQUENCE: 150

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Asp
 1 5 10 15

Ser Leu Arg Leu Ser Cys Leu Ala Thr Gly Ser Met Phe Ser Ile Asn
 20 25 30

Ala Trp Gly Trp Tyr Arg Gln Ala Pro Gly Lys Gln Arg Glu Leu Val
 35 40 45

Ala Ser Ile Thr Ser Gly Gly Gly Ser Thr Glu Tyr Ala Glu Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Ser Ala Lys Asn Met Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Asn Ala Glu Arg Trp Asp Gly Tyr Ala Leu Gly Tyr Ser Pro Asn His
 100 105 110

Gly Ser Gly His Arg Pro Tyr Asn Tyr Trp Gly Gln Gly Thr Gln Val
 115 120 125

Thr Val Ser Ser
 130

<210> SEQ ID NO 151
 <211> LENGTH: 120
 <212> TYPE: PRT
 <213> ORGANISM: *Vicugna pacos*

<400> SEQUENCE: 151

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Ser Ile Phe Ser Ile Asn
 20 25 30

Ala Trp Gly Trp Tyr Arg Gln Ala Pro Gly Lys Gln Arg Glu Leu Val
 35 40 45

Ala Glu Ile Thr Ser Ser Gly Ser Thr Asn Tyr Ala Asp Ser Val Lys
 50 55 60

Gly Arg Phe Thr Ile Ser Gly Asp Asn Ala Lys Asn Ser Val Tyr Leu
 65 70 75 80

His Met Asn Asn Leu Glu Pro Glu Asp Thr Ala Val Tyr Tyr Cys Lys
 85 90 95

Ala Val Ala Val Thr Phe Thr Thr Pro Arg Ser Asp Tyr Trp Gly Arg
 100 105 110

Gly Thr Gln Val Thr Val Ser Ser
 115 120

<210> SEQ ID NO 152
 <211> LENGTH: 116

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<212> TYPE: PRT
<213> ORGANISM: Vicugna pacos

<400> SEQUENCE: 152

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1          5          10          15
Ser Leu Arg Leu Ser Cys Ala Pro Ser Gly Ser Ile Ile Ser Ile Asn
20        25        30
Ala Met Ala Trp Tyr Arg Gln Ala Pro Gly Lys Glu Arg Glu Leu Val
35        40        45
Ala Ala Ile Ser Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys
50        55        60
Gly Arg Phe Thr Ile Ser Gly Asp Ile Ala Lys Asn Leu Leu Trp Leu
65        70        75        80
Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Met Tyr Tyr Cys Ala
85        90        95
Pro Gly Gly Gly Trp Arg Pro Gly Ala Trp Gly Gln Gly Thr Gln Val
100       105       110
Thr Val Ser Ser
115

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<210> SEQ ID NO 153
<211> LENGTH: 116
<212> TYPE: PRT
<213> ORGANISM: Vicugna pacos

<400> SEQUENCE: 153

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1          5          10          15
Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Val Ser Thr Ser
20        25        30
Met Ile Asn Trp Ala Arg Gln Val Pro Gly Lys Glu Leu Glu Trp Leu
35        40        45
Val Asp Val Leu Pro Ser Gly Ser Thr Tyr Tyr Ala Asp Pro Val Lys
50        55        60
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Gln Asn Thr Ile Tyr Leu
65        70        75        80
Gln Met Asn Tyr Leu Lys Pro Glu Asp Thr Ala Ile Tyr Tyr Cys Ala
85        90        95
Ile Asn Arg Glu Thr Met Pro Pro Phe Arg Gly Gln Gly Thr Gln Val
100       105       110
Thr Val Ser Ser
115

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<210> SEQ ID NO 154
<211> LENGTH: 121
<212> TYPE: PRT
<213> ORGANISM: Vicugna pacos

<400> SEQUENCE: 154

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1          5          10          15
Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly Phe Pro Phe Ser Ser Ala
20        25        30
Pro Met Ser Trp Val Arg Gln Ala Pro Gly Lys Glu Leu Glu Trp Val
35        40        45
Ser Tyr Ile Gly Tyr Thr Gly Thr Ile Thr Asp Tyr Ala Asn Ser Val

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50	55	60	
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Arg Leu Tyr			
65	70	75	80
Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Phe Cys			
	85	90	95
Ala Gln Gly Tyr Ala Arg Leu Ile Ala Asp Ser Asp Leu Val Arg Gly			
	100	105	110
Gln Gly Thr Gln Val Thr Val Ser Ser			
	115	120	

<210> SEQ ID NO 155

<211> LENGTH: 121

<212> TYPE: PRT

<213> ORGANISM: Vicugna pacos

<400> SEQUENCE: 155

Gln Val Gln Leu Gln Glu Ser Gly Gly Arg Leu Gly Ala Ala Gly Gly			
1	5	10	15
Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly Phe Pro Phe Asn Ile Tyr			
	20	25	30
Pro Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Phe Glu Trp Val			
	35	40	45
Ser Tyr Ile Ser His Gly Gly Thr Thr Thr Asp Tyr Ser Asp Ala Val			
	50	55	60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Arg Leu Tyr			
65	70	75	80
Leu Gln Met Asp Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Phe Cys			
	85	90	95
Ala Gln Gly Tyr Ala Arg Leu Met Thr Asp Ser Glu Leu Val Arg Gly			
	100	105	110
Gln Gly Thr Gln Val Thr Val Ser Ser			
	115	120	

<210> SEQ ID NO 156

<211> LENGTH: 11

<212> TYPE: PRT

<213> ORGANISM: Vicugna pacos

<400> SEQUENCE: 156

Ser Gly Asn Ile Phe Ser Ile Asn Ala Ile Gly	
1	10

<210> SEQ ID NO 157

<211> LENGTH: 11

<212> TYPE: PRT

<213> ORGANISM: Vicugna pacos

<400> SEQUENCE: 157

Ser Gly Arg Thr Phe Ser Arg Asp Ala Met Gly	
1	10

<210> SEQ ID NO 158

<211> LENGTH: 10

<212> TYPE: PRT

<213> ORGANISM: Vicugna pacos

<400> SEQUENCE: 158

Gly Phe Thr Leu Asp Asn Tyr Thr Val Ala	
1	10

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<210> SEQ ID NO 159
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Vicugna pacos

<400> SEQUENCE: 159

Gly Ser Ile Phe Ser Ile Lys Thr Met Gly
1 5 10

<210> SEQ ID NO 160
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Vicugna pacos

<400> SEQUENCE: 160

Gly Asp Thr Phe Asn His Tyr Ser Trp Gly
1 5 10

<210> SEQ ID NO 161
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Vicugna pacos

<400> SEQUENCE: 161

Gly Phe Thr Leu Asp Tyr Tyr Asp Ile Gly
1 5 10

<210> SEQ ID NO 162
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Vicugna pacos

<400> SEQUENCE: 162

Gly Phe Thr Leu Asp Tyr Tyr Ala Ile Gly
1 5 10

<210> SEQ ID NO 163
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Vicugna pacos

<400> SEQUENCE: 163

Gly Phe Thr Asp Asp Asp Tyr Asp Ile Gly
1 5 10

<210> SEQ ID NO 164
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Vicugna pacos

<400> SEQUENCE: 164

Gly Ser Phe Leu Ser Ile Asn His Met Gly
1 5 10

<210> SEQ ID NO 165
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Vicugna pacos

<400> SEQUENCE: 165

Gly Asn Ile Phe Thr Ile Asn Arg Met Gly
1 5 10

<210> SEQ ID NO 166

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<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Vicugna pacos

<400> SEQUENCE: 166

Gly Ser Thr Phe Ser Ile Asn Asn Met Gly
1 5 10

<210> SEQ ID NO 167
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Vicugna pacos

<400> SEQUENCE: 167

Gly Arg Ile Ala Ser Ile Ser Ala Met Gly
1 5 10

<210> SEQ ID NO 168
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Vicugna pacos

<400> SEQUENCE: 168

Pro Gly Phe Lys Leu Asp Tyr Tyr Ala Ile Ala
1 5 10

<210> SEQ ID NO 169
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Vicugna pacos

<400> SEQUENCE: 169

Gly Arg Thr Phe Ser Ile Asn Tyr Met Gly
1 5 10

<210> SEQ ID NO 170
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Vicugna pacos

<400> SEQUENCE: 170

Gly Gly Thr Phe Asp Asp Ser Val Ile Gly
1 5 10

<210> SEQ ID NO 171
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Vicugna pacos

<400> SEQUENCE: 171

Gly Phe Thr Leu Lys Asn His His Ile Gly
1 5 10

<210> SEQ ID NO 172
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Vicugna pacos

<400> SEQUENCE: 172

Gly Arg Ile Phe Ser Ala Tyr Ala Met Gly
1 5 10

<210> SEQ ID NO 173
<211> LENGTH: 10
<212> TYPE: PRT

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<213> ORGANISM: Vicugna pacos

<400> SEQUENCE: 173

Gly Phe Ser Leu Asp Tyr Tyr Ala Ile Gly
1 5 10

<210> SEQ ID NO 174

<211> LENGTH: 13

<212> TYPE: PRT

<213> ORGANISM: Vicugna pacos

<400> SEQUENCE: 174

Gly Arg Thr Phe Ser Asn Tyr Val Asn Tyr Ala Met Gly
1 5 10

<210> SEQ ID NO 175

<211> LENGTH: 10

<212> TYPE: PRT

<213> ORGANISM: Vicugna pacos

<400> SEQUENCE: 175

Gly Asp Thr Phe Ser Asn Tyr Val Met Ala
1 5 10

<210> SEQ ID NO 176

<211> LENGTH: 10

<212> TYPE: PRT

<213> ORGANISM: Vicugna pacos

<400> SEQUENCE: 176

Gly Arg Thr Phe Ser Ser Ala Ala Met Gly
1 5 10

<210> SEQ ID NO 177

<211> LENGTH: 10

<212> TYPE: PRT

<213> ORGANISM: Vicugna pacos

<400> SEQUENCE: 177

Gly Arg Thr Phe Ser Ile Asn Tyr Met Gly
1 5 10

<210> SEQ ID NO 178

<211> LENGTH: 10

<212> TYPE: PRT

<213> ORGANISM: Vicugna pacos

<400> SEQUENCE: 178

Gly Ser Thr Phe Ser Ile Asn Asn Met Gly
1 5 10

<210> SEQ ID NO 179

<211> LENGTH: 10

<212> TYPE: PRT

<213> ORGANISM: Vicugna pacos

<400> SEQUENCE: 179

Gly Ser Ile Val Ser Ile Asn Ala Met Gly
1 5 10

<210> SEQ ID NO 180

<211> LENGTH: 10

<212> TYPE: PRT

<213> ORGANISM: Vicugna pacos

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<400> SEQUENCE: 180

Gly Ser Ile Phe Ser Ile Lys Thr Met Gly
1 5 10

<210> SEQ ID NO 181

<211> LENGTH: 10

<212> TYPE: PRT

<213> ORGANISM: Vicugna pacos

<400> SEQUENCE: 181

Gly Arg Thr Phe Ser Val Asn Ala Met Ala
1 5 10

<210> SEQ ID NO 182

<211> LENGTH: 10

<212> TYPE: PRT

<213> ORGANISM: Vicugna pacos

<400> SEQUENCE: 182

Gly Ser Met Phe Ser Ile Asn Ala Trp Gly
1 5 10

<210> SEQ ID NO 183

<211> LENGTH: 10

<212> TYPE: PRT

<213> ORGANISM: Vicugna pacos

<400> SEQUENCE: 183

Gly Ser Ile Phe Ser Ile Asn Ala Trp Gly
1 5 10

<210> SEQ ID NO 184

<211> LENGTH: 10

<212> TYPE: PRT

<213> ORGANISM: Vicugna pacos

<400> SEQUENCE: 184

Gly Ser Ile Ile Ser Ile Asn Ala Met Ala
1 5 10

<210> SEQ ID NO 185

<211> LENGTH: 10

<212> TYPE: PRT

<213> ORGANISM: Vicugna pacos

<400> SEQUENCE: 185

Gly Phe Thr Val Ser Thr Ser Met Ile Asn
1 5 10

<210> SEQ ID NO 186

<211> LENGTH: 10

<212> TYPE: PRT

<213> ORGANISM: Vicugna pacos

<400> SEQUENCE: 186

Gly Phe Pro Phe Ser Ser Ala Pro Met Ser
1 5 10

<210> SEQ ID NO 187

<211> LENGTH: 10

<212> TYPE: PRT

<213> ORGANISM: Vicugna pacos

<400> SEQUENCE: 187

Gly Phe Pro Phe Asn Ile Tyr Pro Met Ser
1 5 10

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<210> SEQ ID NO 188
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Vicugna pacos
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<400> SEQUENCE: 188

Thr Ile Thr Leu Ser Gly Ser Thr Asn
1 5

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<210> SEQ ID NO 189
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Vicugna pacos
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<400> SEQUENCE: 189

Gly Ile Ser Trp Ser Gly Gly Ser Thr
1 5

```
<210> SEQ ID NO 190
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Vicugna pacos
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<400> SEQUENCE: 190

Cys Ile Ser Ser Ser Gly Gly Ser Thr
1 5

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<210> SEQ ID NO 191
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Vicugna pacos
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<400> SEQUENCE: 191

Ala Ile Thr Ser Gly Gly Ser Thr
1 5

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<210> SEQ ID NO 192
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Vicugna pacos
```

<400> SEQUENCE: 192

Ala Ile Ser Trp Asn Gly Gly Ser
1 5

```
<210> SEQ ID NO 193
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Vicugna pacos
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<400> SEQUENCE: 193

Cys Ile Ser Ser Ile Gly Gly Ser Ala
1 5

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<210> SEQ ID NO 194
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Vicugna pacos
```

<400> SEQUENCE: 194

Cys Ile Ser Tyr Lys Gly Gly Ser Thr
1 5

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<210> SEQ ID NO 195
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Vicugna pacos

<400> SEQUENCE: 195

Cys Ile Ser Ser Ser Asp Gly Ser Thr
1 5

<210> SEQ ID NO 196
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Vicugna pacos

<400> SEQUENCE: 196

Ala Ile Thr Ser Gly Gly Ser Thr
1 5

<210> SEQ ID NO 197
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Vicugna pacos

<400> SEQUENCE: 197

Ala Ile Thr Ser Gly Gly Asn Thr
1 5

<210> SEQ ID NO 198
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Vicugna pacos

<400> SEQUENCE: 198

Gly Ile Thr Gly Gly Asn Thr
1 5

<210> SEQ ID NO 199
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Vicugna pacos

<400> SEQUENCE: 199

Ala Ile Thr Gly Ser Gly Arg Thr
1 5

<210> SEQ ID NO 200
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Vicugna pacos

<400> SEQUENCE: 200

Cys Ile Gly Gly Ser Gly Ser Gly Leu Thr
1 5 10

<210> SEQ ID NO 201
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Vicugna pacos

<400> SEQUENCE: 201

Ala Ile Thr Ser Gly Ser Gly Ser Thr
1 5

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<210> SEQ ID NO 202
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Vicugna pacos

<400> SEQUENCE: 202

Cys Ile Ser Ser Asn Asp Gly Thr Thr
1 5

<210> SEQ ID NO 203
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Vicugna pacos

<400> SEQUENCE: 203

Ser Ile Asn Ser Ser Gly Gly Ser Thr
1 5

<210> SEQ ID NO 204
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Vicugna pacos

<400> SEQUENCE: 204

Ala Ile Ser Arg Ser Gly Asp Ser Thr
1 5

<210> SEQ ID NO 205
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Vicugna pacos

<400> SEQUENCE: 205

Cys Ile Ser Tyr Lys Gly Gly Ser Thr
1 5

<210> SEQ ID NO 206
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Vicugna pacos

<400> SEQUENCE: 206

Ser Ile Ser Trp Ser Ser Val Thr Thr
1 5

<210> SEQ ID NO 207
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Vicugna pacos

<400> SEQUENCE: 207

Ala Ile Arg Leu Ser Gly Ala Arg
1 5

<210> SEQ ID NO 208
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Vicugna pacos

<400> SEQUENCE: 208

Leu Ile Asn Leu Asp Asp Gly Glu Thr
1 5

<210> SEQ ID NO 209
<211> LENGTH: 9

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<212> TYPE: PRT
<213> ORGANISM: Vicugna pacos

<400> SEQUENCE: 209

Ala Ile Thr Ser Gly Ser Gly Ser Thr
1 5

<210> SEQ ID NO 210
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Vicugna pacos

<400> SEQUENCE: 210

Gly Ile Thr Gly Gly Asn Thr
1 5

<210> SEQ ID NO 211
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Vicugna pacos

<400> SEQUENCE: 211

Leu Val Thr Gly Ser Gly Arg Thr
1 5

<210> SEQ ID NO 212
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Vicugna pacos

<400> SEQUENCE: 212

Ala Val Ser Ser Gly Gly Ser Thr
1 5

<210> SEQ ID NO 213
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Vicugna pacos

<400> SEQUENCE: 213

Ser Ile Thr Ser Ser Gly Leu Asp Thr
1 5

<210> SEQ ID NO 214
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Vicugna pacos

<400> SEQUENCE: 214

Ser Ile Thr Ser Gly Gly Gly Ser Thr
1 5

<210> SEQ ID NO 215
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Vicugna pacos

<400> SEQUENCE: 215

Glu Ile Thr Ser Ser Gly Ser Thr
1 5

<210> SEQ ID NO 216
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Vicugna pacos

-continued

<400> SEQUENCE: 216

Ala Ile Ser Ser Gly Gly Ser Thr
1 5

<210> SEQ ID NO 217

<211> LENGTH: 8

<212> TYPE: PRT

<213> ORGANISM: Vicugna pacos

<400> SEQUENCE: 217

Asp Val Leu Pro Ser Gly Ser Thr
1 5

<210> SEQ ID NO 218

<211> LENGTH: 9

<212> TYPE: PRT

<213> ORGANISM: Vicugna pacos

<400> SEQUENCE: 218

Tyr Ile Gly Tyr Thr Gly Thr Ile Thr
1 5

<210> SEQ ID NO 219

<211> LENGTH: 9

<212> TYPE: PRT

<213> ORGANISM: Vicugna pacos

<400> SEQUENCE: 219

Tyr Ile Ser His Gly Gly Thr Thr Thr
1 5

<210> SEQ ID NO 220

<211> LENGTH: 11

<212> TYPE: PRT

<213> ORGANISM: Vicugna pacos

<400> SEQUENCE: 220

Asn Thr Tyr Ser Asp Ser Asp Val Tyr Gly Tyr
1 5 10

<210> SEQ ID NO 221

<211> LENGTH: 15

<212> TYPE: PRT

<213> ORGANISM: Vicugna pacos

<400> SEQUENCE: 221

Ser Ser Ile Tyr Gly Ser Ala Val Val Asp Gly Leu Tyr Asp Tyr
1 5 10 15

<210> SEQ ID NO 222

<211> LENGTH: 24

<212> TYPE: PRT

<213> ORGANISM: Vicugna pacos

<400> SEQUENCE: 222

Glu Arg Ala Pro Pro Tyr Tyr Ser Gly Tyr Tyr Phe Phe Asp Ser Thr
1 5 10 15

Cys Val Ala Ala Ser Tyr Asp Tyr
20

<210> SEQ ID NO 223

<211> LENGTH: 13

<212> TYPE: PRT

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<213> ORGANISM: Vicugna pacos

<400> SEQUENCE: 223

Asp Gly Val Val Ala Trp Asp Gln Pro Tyr Asp Asn Tyr
 1 5 10

<210> SEQ ID NO 224

<211> LENGTH: 17

<212> TYPE: PRT

<213> ORGANISM: Vicugna pacos

<400> SEQUENCE: 224

Asp Arg Arg Pro Tyr Asn Asp Trp Trp Asp Asp Trp Ser Trp Trp Val
 1 5 10 15

Tyr

<210> SEQ ID NO 225

<211> LENGTH: 18

<212> TYPE: PRT

<213> ORGANISM: Vicugna pacos

<400> SEQUENCE: 225

Glu Ala Gln Thr Pro Tyr Asn Asp Gly Asp Cys Thr Arg Ala Ser Tyr
 1 5 10 15

Asp Tyr

<210> SEQ ID NO 226

<211> LENGTH: 9

<212> TYPE: PRT

<213> ORGANISM: Vicugna pacos

<400> SEQUENCE: 226

Gly Phe Val Cys Tyr Asn Tyr Asp Tyr
 1 5

<210> SEQ ID NO 227

<211> LENGTH: 22

<212> TYPE: PRT

<213> ORGANISM: Vicugna pacos

<400> SEQUENCE: 227

Asp Phe Phe Arg Trp Asp Ser Gly Ser Tyr Tyr Val Arg Gly Cys Arg
 1 5 10 15

His Ala Thr Tyr Asp Tyr
 20

<210> SEQ ID NO 228

<211> LENGTH: 11

<212> TYPE: PRT

<213> ORGANISM: Vicugna pacos

<400> SEQUENCE: 228

Asp Ala Leu Thr Met Leu Pro Pro Phe Asp Phe
 1 5 10

<210> SEQ ID NO 229

<211> LENGTH: 12

<212> TYPE: PRT

<213> ORGANISM: Vicugna pacos

<400> SEQUENCE: 229

Ala Ile Val Thr Met Thr Ser Pro Tyr Ser Asp Tyr
 1 5 10

-continued

<210> SEQ ID NO 230
<211> LENGTH: 5
<212> TYPE: PRT
<213> ORGANISM: Vicugna pacos

<400> SEQUENCE: 230

Asn Trp Gly Ala Tyr
1 5

<210> SEQ ID NO 231
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Vicugna pacos

<400> SEQUENCE: 231

Leu Met Val Asp Tyr Gly Leu Gly Leu Gly Thr Asp Tyr
1 5 10

<210> SEQ ID NO 232
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Vicugna pacos

<400> SEQUENCE: 232

Asp Thr Tyr Tyr Tyr Cys Ser Lys Arg Val Trp Arg Asn Asp Tyr Gly
1 5 10 15

Ser

<210> SEQ ID NO 233
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Vicugna pacos

<400> SEQUENCE: 233

Asp Met Asp Ser Ser Leu Ser Gly Gly Tyr Val Asp Val
1 5 10

<210> SEQ ID NO 234
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Vicugna pacos

<400> SEQUENCE: 234

Glu Thr Pro Ser Ile Gly Ser Pro Cys Thr Ser Ala Ser Tyr Asp Tyr
1 5 10 15

<210> SEQ ID NO 235
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Vicugna pacos

<400> SEQUENCE: 235

Leu Arg Arg Tyr Tyr Gly Leu Asn Leu Asp Pro Gly Ser Tyr Asp Tyr
1 5 10 15

<210> SEQ ID NO 236
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Vicugna pacos

<400> SEQUENCE: 236

Arg Thr Val Ser Ala Pro Pro Ser Ala Ala Trp Gly Tyr Gly Tyr
1 5 10 15

-continued

<210> SEQ ID NO 237
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Vicugna pacos

<400> SEQUENCE: 237

Gly Phe Val Cys Tyr Asn Tyr Asp Tyr
1 5

<210> SEQ ID NO 238
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Vicugna pacos

<400> SEQUENCE: 238

His Leu Ala Gln Tyr Ser Asp Tyr Ala Tyr Arg Asp Pro His Gln Phe
1 5 10 15

Gly Ala

<210> SEQ ID NO 239
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Vicugna pacos

<400> SEQUENCE: 239

Gly His Thr Trp Gly Gln Tyr Ala Tyr
1 5

<210> SEQ ID NO 240
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Vicugna pacos

<400> SEQUENCE: 240

Arg Gly Arg Phe Asp Asp Asn Tyr Glu Tyr
1 5 10

<210> SEQ ID NO 241
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Vicugna pacos

<400> SEQUENCE: 241

Asp Met Asp Ser Ser Leu Ser Gly Gly Tyr Val Asp Val
1 5 10

<210> SEQ ID NO 242
<211> LENGTH: 5
<212> TYPE: PRT
<213> ORGANISM: Vicugna pacos

<400> SEQUENCE: 242

Asn Trp Gly Ala Tyr
1 5

<210> SEQ ID NO 243
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Vicugna pacos

<400> SEQUENCE: 243

Leu Val Ile Gly Pro Leu Glu Gly Tyr Asp Tyr
1 5 10

-continued

<210> SEQ ID NO 244
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Vicugna pacos

<400> SEQUENCE: 244

Asp Gly Val Val Ala Trp Asp Gln Pro Tyr Asp Asn Tyr
1 5 10

<210> SEQ ID NO 245
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Vicugna pacos

<400> SEQUENCE: 245

Glu Arg Trp Asp Asn Gly Met Val Tyr
1 5

<210> SEQ ID NO 246
<211> LENGTH: 23
<212> TYPE: PRT
<213> ORGANISM: Vicugna pacos

<400> SEQUENCE: 246

Glu Arg Trp Asp Gly Tyr Ala Leu Gly Tyr Ser Pro Asn His Gly Ser
1 5 10 15

Gly His Arg Pro Tyr Asn Tyr
20

<210> SEQ ID NO 247
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Vicugna pacos

<400> SEQUENCE: 247

Val Ala Val Thr Phe Thr Thr Pro Arg Ser Asp Tyr
1 5 10

<210> SEQ ID NO 248
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Vicugna pacos

<400> SEQUENCE: 248

Gly Gly Gly Trp Arg Pro Gly Ala
1 5

<210> SEQ ID NO 249
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Vicugna pacos

<400> SEQUENCE: 249

Asn Arg Glu Thr Met Pro Pro Phe
1 5

<210> SEQ ID NO 250
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Vicugna pacos

<400> SEQUENCE: 250

Gly Tyr Ala Arg Leu Ile Ala Asp Ser Asp Leu Val

-continued

1 5 10

<210> SEQ ID NO 251
 <211> LENGTH: 12
 <212> TYPE: PRT
 <213> ORGANISM: Vicugna pacos

<400> SEQUENCE: 251

Gly Tyr Ala Arg Leu Met Thr Asp Ser Glu Leu Val
 1 5 10

<210> SEQ ID NO 252
 <211> LENGTH: 22
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Primer

<400> SEQUENCE: 252

gtcctggctc tcttctacaa gg 22

<210> SEQ ID NO 253
 <211> LENGTH: 23
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Primer

<400> SEQUENCE: 253

ggtacgtgct gttgaactgt tcc 23

<210> SEQ ID NO 254
 <211> LENGTH: 24
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Primer
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (24)..(24)
 <223> OTHER INFORMATION: n can be a or g

<400> SEQUENCE: 254

gatgtgcagc tgcaggagtc tggc 24

<210> SEQ ID NO 255
 <211> LENGTH: 30
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Primer

<400> SEQUENCE: 255

ctagtgcggc cgctgaggag acggtgacct 30

<210> SEQ ID NO 256
 <211> LENGTH: 10
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: HA tag

<400> SEQUENCE: 256

Tyr Pro Tyr Asp Val Pro Asp Tyr Gly Ser
 1 5 10

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<210> SEQ ID NO 257
<211> LENGTH: 19
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: C-terminal extension

<400> SEQUENCE: 257

Ala Ala Ala Tyr Pro Tyr Asp Val Pro Asp Tyr Gly Ser His His His
1           5           10           15

His His His

<210> SEQ ID NO 258
<211> LENGTH: 1456
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 258

Met Arg Leu Pro Leu Leu Leu Val Phe Ala Ser Val Ile Pro Gly Ala
1           5           10           15

Val Leu Leu Leu Asp Thr Arg Gln Phe Leu Ile Tyr Asn Glu Asp His
                20           25           30

Lys Arg Cys Val Asp Ala Val Ser Pro Ser Ala Val Gln Thr Ala Ala
                35           40           45

Cys Asn Gln Asp Ala Glu Ser Gln Lys Phe Arg Trp Val Ser Glu Ser
                50           55           60

Gln Ile Met Ser Val Ala Phe Lys Leu Cys Leu Gly Val Pro Ser Lys
65           70           75           80

Thr Asp Trp Val Ala Ile Thr Leu Tyr Ala Cys Asp Ser Lys Ser Glu
                85           90           95

Phe Gln Lys Trp Glu Cys Lys Asn Asp Thr Leu Leu Gly Ile Lys Gly
                100          105          110

Glu Asp Leu Phe Phe Asn Tyr Gly Asn Arg Gln Glu Lys Asn Ile Met
                115          120          125

Leu Tyr Lys Gly Ser Gly Leu Trp Ser Arg Trp Lys Ile Tyr Gly Thr
130          135          140

Thr Asp Asn Leu Cys Ser Arg Gly Tyr Glu Ala Met Tyr Thr Leu Leu
145          150          155          160

Gly Asn Ala Asn Gly Ala Thr Cys Ala Phe Pro Phe Lys Phe Glu Asn
                165          170          175

Lys Trp Tyr Ala Asp Cys Thr Ser Ala Gly Arg Ser Asp Gly Trp Leu
                180          185          190

Trp Cys Gly Thr Thr Thr Asp Tyr Asp Thr Asp Lys Leu Phe Gly Tyr
195          200          205

Cys Pro Leu Lys Phe Glu Gly Ser Glu Ser Leu Trp Asn Lys Asp Pro
210          215          220

Leu Thr Ser Val Ser Tyr Gln Ile Asn Ser Lys Ser Ala Leu Thr Trp
225          230          235          240

His Gln Ala Arg Lys Ser Cys Gln Gln Gln Asn Ala Glu Leu Leu Ser
                245          250          255

Ile Thr Glu Ile His Glu Gln Thr Tyr Leu Thr Gly Leu Thr Ser Ser
260          265          270

Leu Thr Ser Gly Leu Trp Ile Gly Leu Asn Ser Leu Ser Phe Asn Ser
275          280          285

Gly Trp Gln Trp Ser Asp Arg Ser Pro Phe Arg Tyr Leu Asn Trp Leu
290          295          300

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Pro Gly Ser Pro Ser Ala Glu Pro Gly Lys Ser Cys Val Ser Leu Asn	305	310	315	320
Pro Gly Lys Asn Ala Lys Trp Glu Asn Leu Glu Cys Val Gln Lys Leu		325	330	335
Gly Tyr Ile Cys Lys Lys Gly Asn Thr Thr Leu Asn Ser Phe Val Ile		340	345	350
Pro Ser Glu Ser Asp Val Pro Thr His Cys Pro Ser Gln Trp Trp Pro		355	360	365
Tyr Ala Gly His Cys Tyr Lys Ile His Arg Asp Glu Lys Lys Ile Gln		370	375	380
Arg Asp Ala Leu Thr Thr Cys Arg Lys Glu Gly Gly Asp Leu Thr Ser		385	390	395
Ile His Thr Ile Glu Glu Leu Asp Phe Ile Ile Ser Gln Leu Gly Tyr		405	410	415
Glu Pro Asn Asp Glu Leu Trp Ile Gly Leu Asn Asp Ile Lys Ile Gln		420	425	430
Met Tyr Phe Glu Trp Ser Asp Gly Thr Pro Val Thr Phe Thr Lys Trp		435	440	445
Leu Arg Gly Glu Pro Ser His Glu Asn Asn Arg Gln Glu Asp Cys Val		450	455	460
Val Met Lys Gly Lys Asp Gly Tyr Trp Ala Asp Arg Gly Cys Glu Trp		465	470	475
Pro Leu Gly Tyr Ile Cys Lys Met Lys Ser Arg Ser Gln Gly Pro Glu		485	490	495
Ile Val Glu Val Glu Lys Gly Cys Arg Lys Gly Trp Lys Lys His His		500	505	510
Phe Tyr Cys Tyr Met Ile Gly His Thr Leu Ser Thr Phe Ala Glu Ala		515	520	525
Asn Gln Thr Cys Asn Asn Glu Asn Ala Tyr Leu Thr Thr Ile Glu Asp		530	535	540
Arg Tyr Glu Gln Ala Phe Leu Thr Ser Phe Val Gly Leu Arg Pro Glu		545	550	555
Lys Tyr Phe Trp Thr Gly Leu Ser Asp Ile Gln Thr Lys Gly Thr Phe		565	570	575
Gln Trp Thr Ile Glu Glu Glu Val Arg Phe Thr His Trp Asn Ser Asp		580	585	590
Met Pro Gly Arg Lys Pro Gly Cys Val Ala Met Arg Thr Gly Ile Ala		595	600	605
Gly Gly Leu Trp Asp Val Leu Lys Cys Asp Glu Lys Ala Lys Phe Val		610	615	620
Cys Lys His Trp Ala Glu Gly Val Thr His Pro Pro Lys Pro Thr Thr		625	630	635
Thr Pro Glu Pro Lys Cys Pro Glu Asp Trp Gly Ala Ser Ser Arg Thr		645	650	655
Ser Leu Cys Phe Lys Leu Tyr Ala Lys Gly Lys His Glu Lys Lys Thr		660	665	670
Trp Phe Glu Ser Arg Asp Phe Cys Arg Ala Leu Gly Gly Asp Leu Ala		675	680	685
Ser Ile Asn Asn Lys Glu Glu Gln Gln Thr Ile Trp Arg Leu Ile Thr		690	695	700
Ala Ser Gly Ser Tyr His Lys Leu Phe Trp Leu Gly Leu Thr Tyr Gly		705	710	715
Ser Pro Ser Glu Gly Phe Thr Trp Ser Asp Gly Ser Pro Val Ser Tyr				

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725						730						735				
Glu	Asn	Trp	Ala	Tyr	Gly	Glu	Pro	Asn	Asn	Tyr	Gln	Asn	Val	Glu	Tyr	
			740						745				750			
Cys	Gly	Glu	Leu	Lys	Gly	Asp	Pro	Thr	Met	Ser	Trp	Asn	Asp	Ile	Asn	
			755						760				765			
Cys	Glu	His	Leu	Asn	Asn	Trp	Ile	Cys	Gln	Ile	Gln	Lys	Gly	Gln	Thr	
			770				775					780				
Pro	Lys	Pro	Glu	Pro	Thr	Pro	Ala	Pro	Gln	Asp	Asn	Pro	Pro	Val	Thr	
					790						795				800	
Glu	Asp	Gly	Trp	Val	Ile	Tyr	Lys	Asp	Tyr	Gln	Tyr	Tyr	Phe	Ser	Lys	
				805						810				815		
Glu	Lys	Glu	Thr	Met	Asp	Asn	Ala	Arg	Ala	Phe	Cys	Lys	Arg	Asn	Phe	
			820						825				830			
Gly	Asp	Leu	Val	Ser	Ile	Gln	Ser	Glu	Ser	Glu	Lys	Lys	Phe	Leu	Trp	
			835					840					845			
Lys	Tyr	Val	Asn	Arg	Asn	Asp	Ala	Gln	Ser	Ala	Tyr	Phe	Ile	Gly	Leu	
						855						860				
Leu	Ile	Ser	Leu	Asp	Lys	Lys	Phe	Ala	Trp	Met	Asp	Gly	Ser	Lys	Val	
					870						875				880	
Asp	Tyr	Val	Ser	Trp	Ala	Thr	Gly	Glu	Pro	Asn	Phe	Ala	Asn	Glu	Asp	
				885						890				895		
Glu	Asn	Cys	Val	Thr	Met	Tyr	Ser	Asn	Ser	Gly	Phe	Trp	Asn	Asp	Ile	
				900						905				910		
Asn	Cys	Gly	Tyr	Pro	Asn	Ala	Phe	Ile	Cys	Gln	Arg	His	Asn	Ser	Ser	
							920						925			
Ile	Asn	Ala	Thr	Thr	Val	Met	Pro	Thr	Met	Pro	Ser	Val	Pro	Ser	Gly	
						935						940				
Cys	Lys	Glu	Gly	Trp	Asn	Phe	Tyr	Ser	Asn	Lys	Cys	Phe	Lys	Ile	Phe	
					950						955				960	
Gly	Phe	Met	Glu	Glu	Glu	Arg	Lys	Asn	Trp	Gln	Glu	Ala	Arg	Lys	Ala	
				965						970				975		
Cys	Ile	Gly	Phe	Gly	Gly	Asn	Leu	Val	Ser	Ile	Gln	Asn	Glu	Lys	Glu	
				980					985					990		
Gln	Ala	Phe	Leu	Thr	Tyr	His	Met	Lys	Asp	Ser	Thr	Phe	Ser	Ala	Trp	
							1000						1005			
Thr	Gly	Leu	Asn	Asp	Val	Asn	Ser	Glu	His	Thr	Phe	Leu	Trp	Thr		
						1015						1020				
Asp	Gly	Arg	Gly	Val	His	Tyr	Thr	Asn	Trp	Gly	Lys	Gly	Tyr	Pro		
						1030						1035				
Gly	Gly	Arg	Arg	Ser	Ser	Leu	Ser	Tyr	Glu	Asp	Ala	Asp	Cys	Val		
						1045						1050				
Val	Ile	Ile	Gly	Gly	Ala	Ser	Asn	Glu	Ala	Gly	Lys	Trp	Met	Asp		
						1060						1065				
Asp	Thr	Cys	Asp	Ser	Lys	Arg	Gly	Tyr	Ile	Cys	Gln	Thr	Arg	Ser		
						1075						1080				
Asp	Pro	Ser	Leu	Thr	Asn	Pro	Pro	Ala	Thr	Ile	Gln	Thr	Asp	Gly		
						1090						1095				
Phe	Val	Lys	Tyr	Gly	Lys	Ser	Ser	Tyr	Ser	Leu	Met	Arg	Gln	Lys		
						1105						1110				
Phe	Gln	Trp	His	Glu	Ala	Glu	Thr	Tyr	Cys	Lys	Leu	His	Asn	Ser		
						1120						1125				
Leu	Ile	Ala	Ser	Ile	Leu	Asp	Pro	Tyr	Ser	Asn	Ala	Phe	Ala	Trp		
						1135						1140				

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Leu Gln Met Glu Thr Ser Asn Glu Arg Val Trp Ile Ala Leu Asn	
1145 1150 1155	
Ser Asn Leu Thr Asp Asn Gln Tyr Thr Trp Thr Asp Lys Trp Arg	
1160 1165 1170	
Val Arg Tyr Thr Asn Trp Ala Ala Asp Glu Pro Lys Leu Lys Ser	
1175 1180 1185	
Ala Cys Val Tyr Leu Asp Leu Asp Gly Tyr Trp Lys Thr Ala His	
1190 1195 1200	
Cys Asn Glu Ser Phe Tyr Phe Leu Cys Lys Arg Ser Asp Glu Ile	
1205 1210 1215	
Pro Ala Thr Glu Pro Pro Gln Leu Pro Gly Arg Cys Pro Glu Ser	
1220 1225 1230	
Asp His Thr Ala Trp Ile Pro Phe His Gly His Cys Tyr Tyr Ile	
1235 1240 1245	
Glu Ser Ser Tyr Thr Arg Asn Trp Gly Gln Ala Ser Leu Glu Cys	
1250 1255 1260	
Leu Arg Met Gly Ser Ser Leu Val Ser Ile Glu Ser Ala Ala Glu	
1265 1270 1275	
Ser Ser Phe Leu Ser Tyr Arg Val Glu Pro Leu Lys Ser Lys Thr	
1280 1285 1290	
Asn Phe Trp Ile Gly Leu Phe Arg Asn Val Glu Gly Thr Trp Leu	
1295 1300 1305	
Trp Ile Asn Asn Ser Pro Val Ser Phe Val Asn Trp Asn Thr Gly	
1310 1315 1320	
Asp Pro Ser Gly Glu Arg Asn Asp Cys Val Ala Leu His Ala Ser	
1325 1330 1335	
Ser Gly Phe Trp Ser Asn Ile His Cys Ser Ser Tyr Lys Gly Tyr	
1340 1345 1350	
Ile Cys Lys Arg Pro Lys Ile Ile Asp Ala Lys Pro Thr His Glu	
1355 1360 1365	
Leu Leu Thr Thr Lys Ala Asp Thr Arg Lys Met Asp Pro Ser Lys	
1370 1375 1380	
Pro Ser Ser Asn Val Ala Gly Val Val Ile Ile Val Ile Leu Leu	
1385 1390 1395	
Ile Leu Thr Gly Ala Gly Leu Ala Ala Tyr Phe Phe Tyr Lys Lys	
1400 1405 1410	
Arg Arg Val His Leu Pro Gln Glu Gly Ala Phe Glu Asn Thr Leu	
1415 1420 1425	
Tyr Phe Asn Ser Gln Ser Ser Pro Gly Thr Ser Asp Met Lys Asp	
1430 1435 1440	
Leu Val Gly Asn Ile Glu Gln Asn Glu His Ser Val Ile	
1445 1450 1455	

<210> SEQ ID NO 259

<211> LENGTH: 1371

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 259

Leu Leu Asp Thr Arg Gln Phe Leu Ile Tyr Asn Glu Asp His Lys Arg	
1 5 10 15	
Cys Val Asp Ala Val Ser Pro Ser Ala Val Gln Thr Ala Ala Cys Asn	
20 25 30	
Gln Asp Ala Glu Ser Gln Lys Phe Arg Trp Val Ser Glu Ser Gln Ile	

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35	40	45
Met Ser Val Ala Phe Lys	Leu Cys Leu Gly Val	Pro Ser Lys Thr Asp
50	55	60
Trp Val Ala Ile Thr Leu	Tyr Ala Cys Asp Ser	Lys Ser Glu Phe Gln
65	70	75
Lys Trp Glu Cys Lys Asn Asp	Thr Leu Leu Gly Ile	Lys Gly Glu Asp
	85	90
Leu Phe Phe Asn Tyr Gly	Asn Arg Gln Glu Lys	Asn Ile Met Leu Tyr
	100	105
Lys Gly Ser Gly Leu Trp	Ser Arg Trp Lys Ile Tyr	Gly Thr Thr Asp
	115	120
Asn Leu Cys Ser Arg Gly	Tyr Glu Ala Met Tyr	Thr Leu Leu Gly Asn
	130	135
Ala Asn Gly Ala Thr Cys	Ala Phe Pro Phe Lys	Phe Glu Asn Lys Trp
145	150	155
Tyr Ala Asp Cys Thr Ser	Ala Gly Arg Ser Asp	Gly Trp Leu Trp Cys
	165	170
Gly Thr Thr Thr Asp Tyr	Asp Thr Asp Lys Leu	Phe Gly Tyr Cys Pro
	180	185
Leu Lys Phe Glu Gly Ser	Glu Ser Leu Trp Asn	Lys Asp Pro Leu Thr
	195	200
Ser Val Ser Tyr Gln Ile	Asn Ser Lys Ser Ala	Leu Thr Trp His Gln
	210	215
Ala Arg Lys Ser Cys Gln	Gln Gln Asn Ala Glu	Leu Leu Ser Ile Thr
225	230	235
Glu Ile His Glu Gln Thr	Tyr Leu Thr Gly Leu	Thr Ser Ser Leu Thr
	245	250
Ser Gly Leu Trp Ile Gly	Leu Asn Ser Leu Ser	Phe Asn Ser Gly Trp
	260	265
Gln Trp Ser Asp Arg Ser	Pro Phe Arg Tyr Leu	Asn Trp Leu Pro Gly
	275	280
Ser Pro Ser Ala Glu Pro	Gly Lys Ser Cys Val	Ser Leu Asn Pro Gly
	290	295
Lys Asn Ala Lys Trp Glu	Asn Leu Glu Cys Val	Gln Lys Leu Gly Tyr
305	310	315
Ile Cys Lys Lys Gly Asn	Thr Thr Leu Asn Ser	Phe Val Ile Pro Ser
	325	330
Glu Ser Asp Val Pro Thr	His Cys Pro Ser Gln	Trp Trp Pro Tyr Ala
	340	345
Gly His Cys Tyr Lys Ile	His Arg Asp Glu Lys	Lys Ile Gln Arg Asp
	355	360
Ala Leu Thr Thr Cys Arg	Lys Glu Gly Gly Asp	Leu Ala Ser Ile His
	370	375
Thr Ile Glu Glu Phe Asp	Phe Ile Ile Ser Gln	Leu Gly Tyr Glu Pro
385	390	395
Asn Asp Glu Leu Trp Ile	Gly Leu Asn Asp Ile	Lys Ile Gln Met Tyr
	405	410
Phe Glu Trp Ser Asp Gly	Thr Pro Val Thr Phe	Thr Lys Trp Leu Arg
	420	425
Gly Glu Pro Ser His Glu	Asn Asn Arg Gln Glu	Asp Cys Val Val Met
	435	440
Lys Gly Lys Asp Gly Tyr	Trp Ala Asp Arg Gly	Cys Glu Trp Pro Leu
450	455	460

Gly 465	Tyr	Ile	Cys	Lys	Met 470	Lys	Ser	Arg	Ser	Gln 475	Gly	Pro	Glu	Ile	Val 480
Glu	Val	Glu	Lys	Gly 485	Cys	Arg	Lys	Gly	Trp 490	Lys	Lys	His	His	Phe	Tyr 495
Cys	Tyr	Met	Ile	Gly 500	His	Thr	Leu	Ser 505	Thr	Phe	Ala	Glu	Ala	Asn	Gln
Thr	Cys	Asn	Asn	Glu 515	Asn	Ala	Tyr	Leu 520	Thr	Thr	Ile	Glu 525	Asp	Arg	Tyr
Glu	Gln	Ala	Phe	Leu 530	Thr	Ser 535	Phe	Val	Gly	Leu	Arg 540	Pro	Glu	Lys	Tyr
Phe 545	Trp	Thr	Gly	Leu 550	Ser	Asp	Ile	Gln	Thr	Lys 555	Gly	Thr	Phe	Gln	Trp 560
Thr	Ile	Glu	Glu	Glu 565	Val	Arg	Phe	Thr	His 570	Trp	Asn	Ser	Asp	Met	Pro
Gly	Arg	Lys	Pro 580	Gly	Cys	Val	Ala	Met 585	Arg	Thr	Gly	Ile	Ala	Gly	Gly
Leu	Trp	Asp	Val	Leu 595	Lys	Cys	Asp 600	Glu	Lys	Ala	Lys	Phe 605	Val	Cys	Lys
His 610	Trp	Ala	Glu	Gly	Val	Thr 615	His	Pro	Pro	Lys 620	Pro	Thr	Thr	Thr	Pro
Glu 625	Pro	Lys	Cys	Pro 630	Glu	Asp	Trp	Gly	Ala	Ser 635	Ser	Arg	Thr	Ser	Leu 640
Cys	Phe	Lys	Leu 645	Tyr	Ala	Lys	Gly	Lys	His 650	Glu	Lys	Lys	Thr	Trp	Phe 655
Glu	Ser	Arg	Asp 660	Phe	Cys	Arg	Ala	Leu 665	Gly	Gly	Asp	Leu 670	Ala	Ser	Ile
Asn	Asn	Lys	Glu 675	Glu	Gln	Gln	Thr 680	Ile	Trp	Arg	Leu	Ile 685	Thr	Ala	Ser
Gly 690	Ser	Tyr	His	Lys	Leu 695	Phe	Trp	Leu	Gly	Leu	Thr 700	Tyr	Gly	Ser	Pro
Ser 705	Glu	Gly	Phe	Thr 710	Trp	Ser	Asp	Gly	Ser	Pro 715	Val	Ser	Tyr	Glu	Asn 720
Trp	Ala	Tyr	Gly 725	Glu	Pro	Asn	Asn	Tyr	Gln 730	Asn	Val	Glu	Tyr	Cys	Gly 735
Glu	Leu	Lys	Gly 740	Asp	Pro	Thr	Met	Ser 745	Trp	Asn	Asp	Ile 750	Asn	Cys	Glu
His	Leu	Asn	Asn 755	Trp	Ile	Cys	Gln 760	Ile	Gln	Lys	Gly	Gln 765	Thr	Pro	Lys
Pro 770	Glu	Pro	Thr	Pro	Ala	Pro 775	Gln	Asp	Asn	Pro 780	Pro	Val	Thr	Glu	Asp
Gly 785	Trp	Val	Ile	Tyr	Lys 790	Asp	Tyr	Gln	Tyr	Tyr 795	Phe	Ser	Lys	Glu	Lys 800
Glu	Thr	Met	Asp 805	Asn	Ala	Arg	Ala	Phe	Cys 810	Lys	Arg	Asn	Phe	Gly	Asp 815
Leu	Val	Ser	Ile 820	Gln	Ser	Glu	Ser	Glu 825	Lys	Lys	Phe	Leu 830	Trp	Lys	Tyr
Val	Asn	Arg	Asn 835	Asp	Ala	Gln	Ser 840	Ala	Tyr	Phe	Ile	Gly 845	Leu	Leu	Ile
Ser 850	Leu	Asp	Lys	Lys	Phe 855	Ala	Trp	Met	Asp	Gly	Ser	Lys 860	Val	Asp	Tyr
Val 865	Ser	Trp	Ala	Thr 870	Gly	Glu	Pro	Asn	Phe	Ala 875	Asn	Glu	Asp	Glu	Asn 880

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Cys	Val	Thr	Met	Tyr	Ser	Asn	Ser	Gly	Phe	Trp	Asn	Asp	Ile	Asn	Cys	885	890	895
Gly	Tyr	Pro	Asn	Ala	Phe	Ile	Cys	Gln	Arg	His	Asn	Ser	Ser	Ile	Asn	900	905	910
Ala	Thr	Thr	Val	Met	Pro	Thr	Met	Pro	Ser	Val	Pro	Ser	Gly	Cys	Lys	915	920	925
Glu	Gly	Trp	Asn	Phe	Tyr	Ser	Asn	Lys	Cys	Phe	Lys	Ile	Phe	Gly	Phe	930	935	940
Met	Glu	Glu	Glu	Arg	Lys	Asn	Trp	Gln	Glu	Ala	Arg	Lys	Ala	Cys	Ile	945	950	955
Gly	Phe	Gly	Gly	Asn	Leu	Val	Ser	Ile	Gln	Asn	Glu	Lys	Glu	Gln	Ala	965	970	975
Phe	Leu	Thr	Tyr	His	Met	Lys	Asp	Ser	Thr	Phe	Ser	Ala	Trp	Thr	Gly	980	985	990
Leu	Asn	Asp	Val	Asn	Ser	Glu	His	Thr	Phe	Leu	Trp	Thr	Asp	Gly	Arg	995	1000	1005
Gly	Val	His	Tyr	Thr	Asn	Trp	Gly	Lys	Gly	Tyr	Pro	Gly	Gly	Arg		1010	1015	1020
Arg	Ser	Ser	Leu	Ser	Tyr	Glu	Asp	Ala	Asp	Cys	Val	Val	Ile	Ile		1025	1030	1035
Gly	Gly	Ala	Ser	Asn	Glu	Ala	Gly	Lys	Trp	Met	Asp	Asp	Thr	Cys		1040	1045	1050
Asp	Ser	Lys	Arg	Gly	Tyr	Ile	Cys	Gln	Thr	Arg	Ser	Asp	Pro	Ser		1055	1060	1065
Leu	Thr	Asn	Pro	Pro	Ala	Thr	Ile	Gln	Thr	Asp	Gly	Phe	Val	Lys		1070	1075	1080
Tyr	Gly	Lys	Ser	Ser	Tyr	Ser	Leu	Met	Arg	Gln	Lys	Phe	Gln	Trp		1085	1090	1095
His	Glu	Ala	Glu	Thr	Tyr	Cys	Lys	Leu	His	Asn	Ser	Leu	Ile	Ala		1100	1105	1110
Ser	Ile	Leu	Asp	Pro	Tyr	Ser	Asn	Ala	Phe	Ala	Trp	Leu	Gln	Met		1115	1120	1125
Glu	Thr	Ser	Asn	Glu	Arg	Val	Trp	Ile	Ala	Leu	Asn	Ser	Asn	Leu		1130	1135	1140
Thr	Asp	Asn	Gln	Tyr	Thr	Trp	Thr	Asp	Lys	Trp	Arg	Val	Arg	Tyr		1145	1150	1155
Thr	Asn	Trp	Ala	Ala	Asp	Glu	Pro	Lys	Leu	Lys	Ser	Ala	Cys	Val		1160	1165	1170
Tyr	Leu	Asp	Leu	Asp	Gly	Tyr	Trp	Lys	Thr	Ala	His	Cys	Asn	Glu		1175	1180	1185
Ser	Phe	Tyr	Phe	Leu	Cys	Lys	Arg	Ser	Asp	Glu	Ile	Pro	Ala	Thr		1190	1195	1200
Glu	Pro	Pro	Gln	Leu	Pro	Gly	Arg	Cys	Pro	Glu	Ser	Asp	His	Thr		1205	1210	1215
Ala	Trp	Ile	Pro	Phe	His	Gly	His	Cys	Tyr	Tyr	Ile	Glu	Ser	Ser		1220	1225	1230
Tyr	Thr	Arg	Asn	Trp	Gly	Gln	Ala	Ser	Leu	Glu	Cys	Leu	Arg	Met		1235	1240	1245
Gly	Ser	Ser	Leu	Val	Ser	Ile	Glu	Ser	Ala	Ala	Glu	Ser	Ser	Phe		1250	1255	1260
Leu	Ser	Tyr	Arg	Val	Glu	Pro	Leu	Lys	Ser	Lys	Thr	Asn	Phe	Trp		1265	1270	1275
Ile	Gly	Leu	Phe	Arg	Asn	Val	Glu	Gly	Thr	Trp	Leu	Trp	Ile	Asn				

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1280	1285	1290
Asn Ser Pro Val Ser Phe Val Asn Trp Asn Thr Gly Asp Pro Ser		
1295	1300	1305
Gly Glu Arg Asn Asp Cys Val Ala Leu His Ala Ser Ser Gly Phe		
1310	1315	1320
Trp Ser Asn Ile His Cys Ser Ser Tyr Lys Gly Tyr Ile Cys Lys		
1325	1330	1335
Arg Pro Lys Ile Ile Asp Ala Lys Pro Thr His Glu Leu Leu Thr		
1340	1345	1350
Thr Lys Ala Asp Thr Arg Lys Met Asp Pro Ser Lys His His His		
1355	1360	1365
His His His		
1370		

<210> SEQ ID NO 260

<211> LENGTH: 1456

<212> TYPE: PRT

<213> ORGANISM: Mus musculus

<400> SEQUENCE: 260

Met Arg Leu Leu Leu Leu Ala Phe Ile Ser Val Ile Pro Val Ser		
1	5	10
Val Gln Leu Leu Asp Ala Arg Gln Phe Leu Ile Tyr Asn Glu Asp His		
	20	25
Lys Arg Cys Val Asp Ala Leu Ser Ala Ile Ser Val Gln Thr Ala Thr		
	35	40
Cys Asn Pro Glu Ala Glu Ser Gln Lys Phe Arg Trp Val Ser Asp Ser		
	50	55
Gln Ile Met Ser Val Ala Phe Lys Leu Cys Leu Gly Val Pro Ser Lys		
	65	70
Thr Asp Trp Ala Ser Val Thr Leu Tyr Ala Cys Asp Ser Lys Ser Glu		
	85	90
Tyr Gln Lys Trp Glu Cys Lys Asn Asp Thr Leu Phe Gly Ile Lys Gly		
	100	105
Thr Glu Leu Tyr Phe Asn Tyr Gly Asn Arg Gln Glu Lys Asn Ile Lys		
	115	120
Leu Tyr Lys Gly Ser Gly Leu Trp Ser Arg Trp Lys Val Tyr Gly Thr		
	130	135
Thr Asp Asp Leu Cys Ser Arg Gly Tyr Glu Ala Met Tyr Ser Leu Leu		
	145	150
Gly Asn Ala Asn Gly Ala Val Cys Ala Phe Pro Phe Lys Phe Glu Asn		
	165	170
Lys Trp Tyr Ala Asp Cys Thr Ser Ala Gly Arg Ser Asp Gly Trp Leu		
	180	185
Trp Cys Gly Thr Thr Thr Asp Tyr Asp Lys Asp Lys Leu Phe Gly Phe		
	195	200
Cys Pro Leu His Phe Glu Gly Ser Glu Arg Leu Trp Asn Lys Asp Pro		
	210	215
Leu Thr Gly Ile Leu Tyr Gln Ile Asn Ser Lys Ser Ala Leu Thr Trp		
	225	230
His Gln Ala Arg Ala Ser Cys Lys Gln Gln Asn Ala Asp Leu Leu Ser		
	245	250
Val Thr Glu Ile His Glu Gln Met Tyr Leu Thr Gly Leu Thr Ser Ser		
	260	265
		270

Leu	Ser	Ser	Gly	Leu	Trp	Ile	Gly	Leu	Asn	Ser	Leu	Val	Arg	Ser
		275				280				285				
Gly	Trp	Gln	Trp	Ala	Gly	Gly	Ser	Pro	Phe	Arg	Tyr	Leu	Asn	Trp
290					295						300			
Pro	Gly	Ser	Pro	Ser	Ser	Glu	Pro	Gly	Lys	Ser	Cys	Val	Ser	Leu
305					310					315				Asn
Pro	Gly	Lys	Asn	Ala	Lys	Trp	Glu	Asn	Leu	Glu	Cys	Val	Gln	Lys
				325					330					Leu
Gly	Tyr	Ile	Cys	Lys	Lys	Gly	Asn	Asn	Thr	Leu	Asn	Pro	Phe	Ile
		340						345					350	Ile
Pro	Ser	Ala	Ser	Asp	Val	Pro	Thr	Gly	Cys	Pro	Asn	Gln	Trp	Trp
355						360					365			Pro
Tyr	Ala	Gly	His	Cys	Tyr	Arg	Ile	His	Arg	Glu	Glu	Lys	Lys	Ile
370						375					380			Gln
Lys	Tyr	Ala	Leu	Gln	Ala	Cys	Arg	Lys	Glu	Gly	Gly	Asp	Leu	Ala
385					390					395				Ser
Ile	His	Ser	Ile	Glu	Glu	Phe	Asp	Phe	Ile	Phe	Ser	Gln	Leu	Gly
				405					410					Tyr
Glu	Pro	Asn	Asp	Glu	Leu	Trp	Ile	Gly	Leu	Asn	Asp	Ile	Lys	Ile
		420						425				430		Gln
Met	Tyr	Phe	Glu	Trp	Ser	Asp	Gly	Thr	Pro	Val	Thr	Phe	Thr	Lys
435						440						445	Trp	
Leu	Pro	Gly	Glu	Pro	Ser	His	Glu	Asn	Asn	Arg	Gln	Glu	Asp	Cys
450						455					460			Val
Val	Met	Lys	Gly	Lys	Asp	Gly	Tyr	Trp	Ala	Asp	Arg	Ala	Cys	Glu
465					470					475				Gln
Pro	Leu	Gly	Tyr	Ile	Cys	Lys	Met	Val	Ser	Gln	Ser	His	Ala	Val
				485					490				495	Val
Pro	Glu	Gly	Ala	Asp	Lys	Gly	Cys	Arg	Lys	Gly	Trp	Lys	Arg	His
		500						505					510	Gly
Phe	Tyr	Cys	Tyr	Leu	Ile	Gly	Ser	Thr	Leu	Ser	Thr	Phe	Thr	Asp
515						520						525	Ala	
Asn	His	Thr	Cys	Thr	Asn	Glu	Lys	Ala	Tyr	Leu	Thr	Thr	Val	Glu
530						535					540			Asp
Arg	Tyr	Glu	Gln	Ala	Phe	Leu	Thr	Ser	Leu	Val	Gly	Leu	Arg	Pro
545					550					555				Glu
Lys	Tyr	Phe	Trp	Thr	Gly	Leu	Ser	Asp	Val	Gln	Asn	Lys	Gly	Thr
		565							570				575	Phe
Arg	Trp	Thr	Val	Asp	Glu	Gln	Val	Gln	Phe	Thr	His	Trp	Asn	Ala
		580						585					590	Asp
Met	Pro	Gly	Arg	Lys	Ala	Gly	Cys	Val	Ala	Met	Lys	Thr	Gly	Val
595						600					605			Ala
Gly	Gly	Leu	Trp	Asp	Val	Leu	Ser	Cys	Glu	Glu	Lys	Ala	Lys	Phe
610						615					620			Val
Cys	Lys	His	Trp	Ala	Glu	Gly	Val	Thr	Arg	Pro	Pro	Glu	Pro	Thr
625					630					635				Thr
Thr	Pro	Glu	Pro	Lys	Cys	Pro	Glu	Asn	Trp	Gly	Thr	Thr	Ser	Lys
		645							650				655</	

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690	695	700
Ser Ser Gly Ser Tyr His Glu Leu Phe Trp Leu Gly Leu Thr Tyr Gly		
705	710	715 720
Ser Pro Ser Glu Gly Phe Thr Trp Ser Asp Gly Ser Pro Val Ser Tyr		
	725	730 735
Glu Asn Trp Ala Tyr Gly Glu Pro Asn Asn Tyr Gln Asn Val Glu Tyr		
	740	745 750
Cys Gly Glu Leu Lys Gly Asp Pro Gly Met Ser Trp Asn Asp Ile Asn		
	755	760 765
Cys Glu His Leu Asn Asn Trp Ile Cys Gln Ile Gln Lys Gly Lys Thr		
	770	775 780
Leu Leu Pro Glu Pro Thr Pro Ala Pro Gln Asp Asn Pro Pro Val Thr		
	785	790 795 800
Ala Asp Gly Trp Val Ile Tyr Lys Asp Tyr Gln Tyr Tyr Phe Ser Lys		
	805	810 815
Glu Lys Glu Thr Met Asp Asn Ala Arg Ala Phe Cys Lys Lys Asn Phe		
	820	825 830
Gly Asp Leu Ala Thr Ile Lys Ser Glu Ser Glu Lys Lys Phe Leu Trp		
	835	840 845
Lys Tyr Ile Asn Lys Asn Gly Gly Gln Ser Pro Tyr Phe Ile Gly Met		
	850	855 860
Leu Ile Ser Met Asp Lys Lys Phe Ile Trp Met Asp Gly Ser Lys Val		
	865	870 875 880
Asp Phe Val Ala Trp Ala Thr Gly Glu Pro Asn Phe Ala Asn Asp Asp		
	885	890 895
Glu Asn Cys Val Thr Met Tyr Thr Asn Ser Gly Phe Trp Asn Asp Ile		
	900	905 910
Asn Cys Gly Tyr Pro Asn Asn Phe Ile Cys Gln Arg His Asn Ser Ser		
	915	920 925
Ile Asn Ala Thr Ala Met Pro Thr Thr Pro Thr Thr Pro Gly Gly Cys		
	930	935 940
Lys Glu Gly Trp His Leu Tyr Lys Asn Lys Cys Phe Lys Ile Phe Gly		
	945	950 955 960
Phe Ala Asn Glu Glu Lys Lys Ser Trp Gln Asp Ala Arg Gln Ala Cys		
	965	970 975
Lys Gly Leu Lys Gly Asn Leu Val Ser Ile Glu Asn Ala Gln Glu Gln		
	980	985 990
Ala Phe Val Thr Tyr His Met Arg Asp Ser Thr Phe Asn Ala Trp Thr		
	995	1000 1005
Gly Leu Asn Asp Ile Asn Ala Glu His Met Phe Leu Trp Thr Ala		
	1010	1015 1020
Gly Gln Gly Val His Tyr Thr Asn Trp Gly Lys Gly Tyr Pro Gly		
	1025	1030 1035
Gly Arg Arg Ser Ser Leu Ser Tyr Glu Asp Ala Asp Cys Val Val		
	1040	1045 1050
Val Ile Gly Gly Asn Ser Arg Glu Ala Gly Thr Trp Met Asp Asp		
	1055	1060 1065
Thr Cys Asp Ser Lys Gln Gly Tyr Ile Cys Gln Thr Gln Thr Asp		
	1070	1075 1080
Pro Ser Leu Pro Val Ser Pro Thr Thr Thr Pro Lys Asp Gly Phe		
	1085	1090 1095
Val Thr Tyr Gly Lys Ser Ser Tyr Ser Leu Met Lys Leu Lys Leu		
	1100	1105 1110

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Pro Trp	His Glu Ala Glu Thr	Tyr Cys Lys Asp His	Thr Ser Leu
1115	1120	1125	
Leu Ala	Ser Ile Leu Asp Pro	Tyr Ser Asn Ala Phe	Ala Trp Met
1130	1135	1140	
Lys Met	His Pro Phe Asn Val	Pro Ile Trp Ile Ala	Leu Asn Ser
1145	1150	1155	
Asn Leu	Thr Asn Asn Glu Tyr	Thr Trp Thr Asp Arg	Trp Arg Val
1160	1165	1170	
Arg Tyr	Thr Asn Trp Gly Ala	Asp Glu Pro Lys Leu	Lys Ser Ala
1175	1180	1185	
Cys Val	Tyr Met Asp Val Asp	Gly Tyr Trp Arg Thr	Ser Tyr Cys
1190	1195	1200	
Asn Glu	Ser Phe Tyr Phe Leu	Cys Lys Lys Ser Asp	Glu Ile Pro
1205	1210	1215	
Ala Thr	Glu Pro Pro Gln Leu	Pro Gly Lys Cys Pro	Glu Ser Glu
1220	1225	1230	
Gln Thr	Ala Trp Ile Pro Phe	Tyr Gly His Cys Tyr	Tyr Phe Glu
1235	1240	1245	
Ser Ser	Phe Thr Arg Ser Trp	Gly Gln Ala Ser Leu	Glu Cys Leu
1250	1255	1260	
Arg Met	Gly Ala Ser Leu Val	Ser Ile Glu Thr Ala	Ala Glu Ser
1265	1270	1275	
Ser Phe	Leu Ser Tyr Arg Val	Glu Pro Leu Lys Ser	Lys Thr Asn
1280	1285	1290	
Phe Trp	Ile Gly Met Phe Arg	Asn Val Glu Gly Lys	Trp Leu Trp
1295	1300	1305	
Leu Asn	Asp Asn Pro Val Ser	Phe Val Asn Trp Lys	Thr Gly Asp
1310	1315	1320	
Pro Ser	Gly Glu Arg Asn Asp	Cys Val Val Leu Ala	Ser Ser Ser
1325	1330	1335	
Gly Leu	Trp Asn Asn Ile His	Cys Ser Ser Tyr Lys	Gly Phe Ile
1340	1345	1350	
Cys Lys	Met Pro Lys Ile Ile	Asp Pro Val Thr Thr	His Ser Ser
1355	1360	1365	
Ile Thr	Thr Lys Ala Asp Gln	Arg Lys Met Asp Pro	Gln Pro Lys
1370	1375	1380	
Gly Ser	Ser Lys Ala Ala Gly	Val Val Thr Val Val	Leu Leu Ile
1385	1390	1395	
Val Ile	Gly Ala Gly Val Ala	Ala Tyr Phe Phe Tyr	Lys Lys Arg
1400	1405	1410	
His Ala	Leu His Ile Pro Gln	Glu Ala Thr Phe Glu	Asn Thr Leu
1415	1420	1425	
Tyr Phe	Asn Ser Asn Leu Ser	Pro Gly Thr Ser Asp	Thr Lys Asp
1430	1435	1440	
Leu Met	Gly Asn Ile Glu Gln	Asn Glu His Ala Ile	Ile
1445	1450	1455	

<210> SEQ ID NO 261

<211> LENGTH: 1376

<212> TYPE: PRT

<213> ORGANISM: Mus musculus

<400> SEQUENCE: 261

Leu Leu Asp Ala Arg Gln Phe Leu Ile Tyr Asn Glu Asp His Lys Arg

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1	5	10	15
Cys Val Asp	Ala Leu Ser	Ala Ile Ser	Val Gln Thr
	20	25	30
Pro Glu Ala	Glu Ser Gln	Lys Phe Arg	Trp Val Ser
	35	40	45
Met Ser Val	Ala Phe Lys	Leu Cys Leu	Gly Val Pro
	50	55	60
Trp Ala Ser	Val Thr Leu	Tyr Ala Cys	Asp Ser Lys
	65	70	75
Lys Trp Glu	Cys Lys Asn	Asp Thr Leu	Phe Gly Ile
	85	90	95
Leu Tyr Phe	Asn Tyr Gly	Asn Arg Gln	Glu Lys Asn
	100	105	110
Lys Gly Ser	Gly Leu Trp	Ser Arg Trp	Lys Val Tyr
	115	120	125
Asp Leu Cys	Ser Arg Gly	Tyr Glu Ala	Met Tyr Ser
	130	135	140
Ala Asn Gly	Ala Val Cys	Ala Phe Pro	Phe Lys Phe
	145	150	155
Tyr Ala Asp	Cys Thr Ser	Ala Gly Arg	Ser Asp Gly
	165	170	175
Gly Thr Thr	Thr Asp Tyr	Asp Lys Asp	Lys Leu Phe
	180	185	190
Leu His Phe	Glu Gly Ser	Glu Arg Leu	Trp Asn Lys
	195	200	205
Gly Ile Leu	Tyr Gln Ile	Asn Ser Lys	Ser Ala Leu
	210	215	220
Ala Arg Ala	Ser Cys Lys	Gln Gln Asn	Ala Asp Leu
	225	230	235
Glu Ile His	Glu Gln Met	Tyr Leu Thr	Gly Leu Thr
	245	250	255
Ser Gly Leu	Trp Ile Gly	Leu Asn Ser	Leu Ser Val
	260	265	270
Gln Trp Ala	Gly Gly Ser	Pro Phe Arg	Tyr Leu Asn
	275	280	285
Ser Pro Ser	Ser Glu Pro	Gly Lys Ser	Cys Val Ser
	290	295	300
Lys Asn Ala	Lys Trp Glu	Asn Leu Glu	Cys Val Gln
	305	310	315
Ile Cys Lys	Lys Gly Asn	Asn Thr Leu	Asn Pro Phe
	325	330	335
Ala Ser Asp	Val Pro Thr	Gly Cys Pro	Asn Gln Trp
	340	345	350
Gly His Cys	Tyr Arg Ile	His Arg Glu	Glu Lys Lys
	355	360	365
Ala Leu Gln	Ala Cys Arg	Lys Glu Gly	Gly Asp Leu
	370	375	380
Ser Ile Glu	Glu Phe Asp	Phe Ile Phe	Ser Gln Leu
	385	390	395
Asn Asp Glu	Leu Trp Ile	Gly Leu Asn	Asp Ile Lys
	405	410	415
Phe Glu Trp	Ser Asp Gly	Thr Pro Val	Thr Phe Thr
	420	425	430

Gly 435	Glu 435	Pro 435	Ser 435	His 435	Glu 440	Asn 440	Asn 440	Arg 440	Gln 445	Glu 445	Asp 445	Cys 445	Val 445	Val 445	Met 445
Lys 450	Gly 450	Lys 450	Asp 450	Gly 455	Tyr 455	Trp 455	Ala 455	Asp 455	Arg 460	Ala 460	Cys 460	Glu 460	Gln 460	Pro 460	Leu 460
Gly 465	Tyr 465	Ile 465	Cys 465	Lys 470	Met 470	Val 470	Ser 470	Gln 470	Ser 475	His 475	Ala 475	Val 475	Val 475	Pro 475	Glu 480
Gly 485	Ala 485	Asp 485	Lys 485	Gly 485	Cys 485	Arg 485	Lys 485	Gly 490	Trp 490	Lys 490	Arg 490	His 490	Gly 495	Phe 495	Tyr 495
Cys 500	Tyr 500	Leu 500	Ile 500	Gly 500	Ser 500	Thr 500	Leu 505	Ser 505	Thr 505	Phe 505	Thr 505	Asp 510	Ala 510	Asn 510	His 510
Thr 515	Cys 515	Thr 515	Asn 515	Glu 515	Lys 515	Ala 515	Tyr 520	Leu 520	Thr 520	Thr 520	Val 520	Glu 525	Asp 525	Arg 525	Tyr 525
Glu 530	Gln 530	Ala 530	Phe 530	Leu 530	Thr 530	Ser 535	Leu 535	Val 535	Gly 535	Leu 540	Arg 540	Pro 540	Glu 540	Lys 540	Tyr 540
Phe 545	Trp 545	Thr 545	Gly 545	Leu 550	Ser 550	Asp 550	Val 550	Gln 550	Asn 555	Lys 555	Gly 555	Thr 555	Phe 555	Arg 555	Trp 560
Thr 565	Val 565	Asp 565	Glu 565	Gln 565	Val 565	Gln 565	Phe 565	Thr 570	His 570	Trp 570	Asn 570	Ala 570	Asp 575	Met 575	Pro 575
Gly 580	Arg 580	Lys 580	Ala 580	Gly 580	Cys 580	Val 580	Ala 585	Met 585	Lys 585	Thr 585	Gly 585	Val 585	Ala 590	Gly 590	Gly 590
Leu 595	Trp 595	Asp 595	Val 595	Leu 595	Ser 595	Cys 595	Glu 600	Glu 600	Lys 600	Ala 600	Lys 600	Phe 605	Val 605	Cys 605	Lys 605
His 610	Trp 610	Ala 610	Glu 610	Gly 610	Val 610	Thr 615	Arg 615	Pro 615	Pro 615	Glu 620	Pro 620	Thr 620	Thr 620	Thr 620	Pro 620
Glu 625	Pro 625	Lys 625	Cys 625	Pro 625	Glu 630	Asn 630	Trp 630	Gly 630	Thr 630	Thr 635	Ser 635	Lys 635	Thr 635	Ser 635	Met 640
Cys 645	Phe 645	Lys 645	Leu 645	Tyr 645	Ala 645	Lys 645	Gly 645	Lys 645	His 650	Glu 650	Lys 650	Lys 650	Thr 650	Trp 655	Phe 655
Glu 660	Ser 660	Arg 660	Asp 660	Phe 660	Cys 660	Lys 660	Ala 660	Ile 665	Gly 665	Gly 665	Glu 665	Leu 665	Ala 670	Ser 670	Ile 670
Lys 675	Ser 675	Lys 675	Asp 675	Glu 675	Gln 675	Gln 675	Val 680	Ile 680	Trp 680	Arg 680	Leu 680	Ile 685	Thr 685	Ser 685	Ser 685
Gly 690	Ser 690	Tyr 690	His 690	Glu 690	Leu 690	Phe 690	Trp 695	Leu 695	Gly 695	Leu 695	Thr 695	Tyr 695	Gly 695	Ser 695	Pro 695
Ser 705	Glu 705	Gly 705	Phe 705	Thr 705	Trp 710	Ser 710	Asp 710	Gly 710	Ser 710	Pro 715	Val 715	Ser 715	Tyr 715	Glu 715	Asn 720
Trp 725	Ala 725	Tyr 725	Gly 725	Glu 725	Pro 725	Asn 725	Asn 725	Tyr 725	Gln 730	Asn 730	Val 730	Glu 730	Tyr 730	Cys 735	Gly 735
Glu 740	Leu 740	Lys 740	Gly 740	Asp 740	Pro 740	Gly 740	Met 740	Ser 745	Trp 745	Asn 745	Asp 745	Ile 745	Asn 745	Cys 745	Glu 745
His 755	Leu 755	Asn 755	Asn 755	Trp 755	Ile 755	Cys 755	Gln 760	Ile 760	Gln 760	Lys 760	Gly 760	Lys 765	Thr 765	Leu 765	Leu 765
Pro 770	Glu 770	Pro 770	Thr 770	Pro 770	Ala 770	Pro 770	Gln 775	Asp 775	Asn 775	Pro 775	Pro 775	Val 775	Thr 775	Ala 775	Asp 775
Gly 785	Trp 785	Val 785	Ile 785	Tyr 785	Lys 790	Asp 790	Tyr 790	Gln 790	Tyr 790	Tyr 795	Phe 795	Ser 795	Lys 795	Glu 795	Lys 800
Glu 805	Thr 805	Met 805	Asp 805	Asn 805	Ala 805	Arg 805	Ala 805	Phe 805	Cys 810	Lys 810	Lys 810	Asn 810	Phe 810	Gly 810	Asp 810
Leu 820	Ala 820	Thr 820	Ile 820	Lys 820	Ser 820										

Ser	Met	Asp	Lys	Lys	Phe	Ile	Trp	Met	Asp	Gly	Ser	Lys	Val	Asp	Phe
850						855					860				
Val	Ala	Trp	Ala	Thr	Gly	Glu	Pro	Asn	Phe	Ala	Asn	Asp	Asp	Glu	Asn
865					870					875					880
Cys	Val	Thr	Met	Tyr	Thr	Asn	Ser	Gly	Phe	Trp	Asn	Asp	Ile	Asn	Cys
				885					890					895	
Gly	Tyr	Pro	Asn	Asn	Phe	Ile	Cys	Gln	Arg	His	Asn	Ser	Ser	Ile	Asn
			900					905					910		
Ala	Thr	Ala	Met	Pro	Thr	Thr	Pro	Thr	Thr	Pro	Gly	Gly	Cys	Lys	Glu
		915					920					925			
Gly	Trp	His	Leu	Tyr	Lys	Asn	Lys	Cys	Phe	Lys	Ile	Phe	Gly	Phe	Ala
930						935					940				
Asn	Glu	Glu	Lys	Lys	Ser	Trp	Gln	Asp	Ala	Arg	Gln	Ala	Cys	Lys	Gly
945					950					955					960
Leu	Lys	Gly	Asn	Leu	Val	Ser	Ile	Glu	Asn	Ala	Gln	Glu	Gln	Ala	Phe
			965						970					975	
Val	Thr	Tyr	His	Met	Arg	Asp	Ser	Thr	Phe	Asn	Ala	Trp	Thr	Gly	Leu
			980					985					990		
Asn	Asp	Ile	Asn	Ala	Glu	His	Met	Phe	Leu	Trp	Thr	Ala	Gly	Gln	Gly
		995					1000					1005			
Val	His	Tyr	Thr	Asn	Trp	Gly	Lys	Gly	Tyr	Pro	Gly	Gly	Arg	Arg	
1010						1015					1020				
Ser	Ser	Leu	Ser	Tyr	Glu	Asp	Ala	Asp	Cys	Val	Val	Val	Ile	Gly	
1025						1030					1035				
Gly	Asn	Ser	Arg	Glu	Ala	Gly	Thr	Trp	Met	Asp	Asp	Thr	Cys	Asp	
1040						1045					1050				
Ser	Lys	Gln	Gly	Tyr	Ile	Cys	Gln	Thr	Gln	Thr	Asp	Pro	Ser	Leu	
1055						1060					1065				
Pro	Val	Ser	Pro	Thr	Thr	Thr	Pro	Lys	Asp	Gly	Phe	Val	Thr	Tyr	
1070						1075					1080				
Gly	Lys	Ser	Ser	Tyr	Ser	Leu	Met	Lys	Leu	Lys	Leu	Pro	Trp	His	
1085						1090					1095				
Glu	Ala	Glu	Thr	Tyr	Cys	Lys	Asp	His	Thr	Ser	Leu	Leu	Ala	Ser	
1100						1105					1110				
Ile	Leu	Asp	Pro	Tyr	Ser	Asn	Ala	Phe	Ala	Trp	Met	Lys	Met	His	
1115						1120					1125				
Pro	Phe	Asn	Val	Pro	Ile	Trp	Ile	Ala	Leu	Asn	Ser	Asn	Leu	Thr	
1130						1135					1140				
Asn	Asn	Glu	Tyr	Thr	Trp	Thr	Asp	Arg	Trp	Arg	Val	Arg	Tyr	Thr	
1145						1150					1155				
Asn	Trp	Gly	Ala	Asp	Glu	Pro	Lys	Leu	Lys	Ser	Ala	Cys	Val	Tyr	
1160						1165					1170				
Met	Asp	Val	Asp	Gly	Tyr	Trp	Arg	Thr	Ser	Tyr	Cys	Asn	Glu	Ser	
1175						1180					1185				
Phe															

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1250	1255	1260
Ser Tyr Arg Val Glu Pro Leu Lys Ser Lys Thr Asn Phe Trp Ile		
1265	1270	1275
Gly Met Phe Arg Asn Val Glu Gly Lys Trp Leu Trp Leu Asn Asp		
1280	1285	1290
Asn Pro Val Ser Phe Val Asn Trp Lys Thr Gly Asp Pro Ser Gly		
1295	1300	1305
Glu Arg Asn Asp Cys Val Val Leu Ala Ser Ser Ser Gly Leu Trp		
1310	1315	1320
Asn Asn Ile His Cys Ser Ser Tyr Lys Gly Phe Ile Cys Lys Met		
1325	1330	1335
Pro Lys Ile Ile Asp Pro Val Thr Thr His Ser Ser Ile Thr Thr		
1340	1345	1350
Lys Ala Asp Gln Arg Lys Met Asp Pro Gln Pro Lys Gly Ser Ser		
1355	1360	1365
Lys Ala His His His His His His		
1370	1375	

<210> SEQ ID NO 262

<211> LENGTH: 1365

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 262

Leu Leu Asp Thr Arg Gln Phe Leu Ile Tyr Asn Glu Asp His Lys Arg		
1	5	10
Cys Val Asp Ala Val Ser Pro Ser Ala Val Gln Thr Ala Ala Cys Asn		
20	25	30
Gln Asp Ala Glu Ser Gln Lys Phe Arg Trp Val Ser Glu Ser Gln Ile		
35	40	45
Met Ser Val Ala Phe Lys Leu Cys Leu Gly Val Pro Ser Lys Thr Asp		
50	55	60
Trp Val Ala Ile Thr Leu Tyr Ala Cys Asp Ser Lys Ser Glu Phe Gln		
65	70	75
Lys Trp Glu Cys Lys Asn Asp Thr Leu Leu Gly Ile Lys Gly Glu Asp		
85	90	95
Leu Phe Phe Asn Tyr Gly Asn Arg Gln Glu Lys Asn Ile Met Leu Tyr		
100	105	110
Lys Gly Ser Gly Leu Trp Ser Arg Trp Lys Ile Tyr Gly Thr Thr Asp		
115	120	125
Asn Leu Cys Ser Arg Gly Tyr Glu Ala Met Tyr Thr Leu Leu Gly Asn		
130	135	140
Ala Asn Gly Ala Thr Cys Ala Phe Pro Phe Lys Phe Glu Asn Lys Trp		
145	150	155
Tyr Ala Asp Cys Thr Ser Ala Gly Arg Ser Asp Gly Trp Leu Trp Cys		
165	170	175
Gly Thr Thr Thr Asp Tyr Asp Thr Asp Lys Leu Phe Gly Tyr Cys Pro		
180	185	190
Leu Lys Phe Glu Gly Ser Glu Ser Leu Trp Asn Lys Asp Pro Leu Thr		
195	200	205
Ser Val Ser Tyr Gln Ile Asn Ser Lys Ser Ala Leu Thr Trp His Gln		
210	215	220
Ala Arg Lys Ser Cys Gln Gln Gln Asn Ala Glu Leu Leu Ser Ile Thr		
225	230	235
		240

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Glu 245	Ile	His	Glu	Gln	Thr	Tyr	Leu	Thr	Gly	Leu	Thr	Ser	Ser	Leu	Thr
Ser	Gly	Leu	Trp	Ile	Gly	Leu	Asn	Ser	Leu	Ser	Phe	Asn	Ser	Gly	Trp
Gln	Trp	Ser	Asp	Arg	Ser	Pro	Phe	Arg	Tyr	Leu	Asn	Trp	Leu	Pro	Gly
Ser	Pro	Ser	Ala	Glu	Pro	Gly	Lys	Ser	Cys	Val	Ser	Leu	Asn	Pro	Gly
Lys 305	Asn	Ala	Lys	Trp	Glu	Asn	Leu	Glu	Cys	Val	Gln	Lys	Leu	Gly	Tyr
Ile	Cys	Lys	Lys	Gly	Asn	Thr	Thr	Leu	Asn	Ser	Phe	Val	Ile	Pro	Ser
Glu	Ser	Asp	Val	Pro	Thr	His	Cys	Pro	Ser	Gln	Trp	Trp	Pro	Tyr	Ala
Gly	His	Cys	Tyr	Lys	Ile	His	Arg	Asp	Glu	Lys	Lys	Ile	Gln	Arg	Asp
Ala 370	Leu	Thr	Thr	Cys	Arg	Lys	Glu	Gly	Gly	Asp	Leu	Thr	Ser	Ile	His
Thr 385	Ile	Glu	Glu	Leu	Asp	Phe	Ile	Ile	Ser	Gln	Leu	Gly	Tyr	Glu	Pro
Asn	Asp	Glu	Leu	Trp	Ile	Gly	Leu	Asn	Asp	Ile	Lys	Ile	Gln	Met	Tyr
Phe	Glu	Trp	Ser	Asp	Gly	Thr	Pro	Val	Thr	Phe	Thr	Lys	Trp	Leu	Arg
Gly	Glu	Pro	Ser	His	Glu	Asn	Asn	Arg	Gln	Glu	Asp	Cys	Val	Val	Met
Lys 450	Gly	Lys	Asp	Gly	Tyr	Trp	Ala	Asp	Arg	Gly	Cys	Glu	Trp	Pro	Leu
Gly 465	Tyr	Ile	Cys	Lys	Met	Lys	Ser	Arg	Ser	Gln	Gly	Pro	Glu	Ile	Val
Glu	Val	Glu	Lys	Gly	Cys	Arg	Lys	Gly	Trp	Lys	Lys	His	His	Phe	Tyr
Cys	Tyr	Met	Ile	Gly	His	Thr	Leu	Ser	Thr	Phe	Ala	Glu	Ala	Asn	Gln
Thr	Cys	Asn	Asn	Glu	Asn	Ala	Tyr	Leu	Thr	Thr	Ile	Glu	Asp	Arg	Tyr
Glu	Gln	Ala	Phe	Leu	Thr	Ser	Phe	Val	Gly	Leu	Arg	Pro	Glu	Lys	Tyr
Phe 545	Trp	Thr	Gly	Leu	Ser	Asp	Ile	Gln	Thr	Lys	Gly	Thr	Phe	Gln	Trp
Thr	Ile	Glu	Glu	Glu	Val	Arg	Phe	Thr	His	Trp	Asn	Ser	Asp	Met	Pro
Gly	Arg	Lys	Pro	Gly	Cys	Val	Ala	Met	Arg	Thr	Gly	Ile	Ala	Gly	Gly
Leu	Trp	Asp	Val	Leu	Lys	Cys	Asp	Glu	Lys	Ala	Lys	Phe	Val	Cys	Lys
His	Trp	Ala	Glu	Gly	Val	Thr	His	Pro	Pro	Lys	Pro	Thr	Thr	Thr	Pro
Glu 625	Pro	Lys	Cys	Pro	Glu	Asp	Trp	Gly	Ala	Ser	Ser	Arg	Thr	Ser	Leu
Cys	Phe	Lys	Leu	Tyr	Ala	Lys	Gly	Lys	His	Glu	Lys	Lys	Thr	Trp	Phe
Glu	Ser	Arg	Asp	Phe	Cys	Arg	Ala	Leu	Gly	Gly	Asp	Leu	Ala	Ser	Ile

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660						665						670					
Asn	Asn	Lys	Glu	Glu	Gln	Gln	Thr	Ile	Trp	Arg	Leu	Ile	Thr	Ala	Ser		
		675					680					685					
Gly	Ser	Tyr	His	Lys	Leu	Phe	Trp	Leu	Gly	Leu	Thr	Tyr	Gly	Ser	Pro		
	690					695					700						
Ser	Glu	Gly	Phe	Thr	Trp	Ser	Asp	Gly	Ser	Pro	Val	Ser	Tyr	Glu	Asn		
	705				710					715					720		
Trp	Ala	Tyr	Gly	Glu	Pro	Asn	Asn	Tyr	Gln	Asn	Val	Glu	Tyr	Cys	Gly		
			725						730					735			
Glu	Leu	Lys	Gly	Asp	Pro	Thr	Met	Ser	Trp	Asn	Asp	Ile	Asn	Cys	Glu		
		740						745					750				
His	Leu	Asn	Asn	Trp	Ile	Cys	Gln	Ile	Gln	Lys	Gly	Gln	Thr	Pro	Lys		
		755					760					765					
Pro	Glu	Pro	Thr	Pro	Ala	Pro	Gln	Asp	Asn	Pro	Pro	Val	Thr	Glu	Asp		
	770					775					780						
Gly	Trp	Val	Ile	Tyr	Lys	Asp	Tyr	Gln	Tyr	Tyr	Phe	Ser	Lys	Glu	Lys		
	785				790					795					800		
Glu	Thr	Met	Asp	Asn	Ala	Arg	Ala	Phe	Cys	Lys	Arg	Asn	Phe	Gly	Asp		
			805						810					815			
Leu	Val	Ser	Ile	Gln	Ser	Glu	Ser	Glu	Lys	Lys	Phe	Leu	Trp	Lys	Tyr		
			820					825					830				
Val	Asn	Arg	Asn	Asp	Ala	Gln	Ser	Ala	Tyr	Phe	Ile	Gly	Leu	Leu	Ile		
		835					840					845					
Ser	Leu	Asp	Lys	Lys	Phe	Ala	Trp	Met	Asp	Gly	Ser	Lys	Val	Asp	Tyr		
	850					855					860						
Val	Ser	Trp	Ala	Thr	Gly	Glu	Pro	Asn	Phe	Ala	Asn	Glu	Asp	Glu	Asn		
	865				870					875					880		
Cys	Val	Thr	Met	Tyr	Ser	Asn	Ser	Gly	Phe	Trp	Asn	Asp	Ile	Asn	Cys		
			885						890					895			
Gly	Tyr	Pro	Asn	Ala	Phe	Ile	Cys	Gln	Arg	His	Asn	Ser	Ser	Ile	Asn		
		900						905						910			
Ala	Thr	Thr	Val	Met	Pro	Thr	Met	Pro	Ser	Val	Pro	Ser	Gly	Cys	Lys		
		915					920						925				
Glu	Gly	Trp	Asn	Phe	Tyr	Ser	Asn	Lys	Cys	Phe	Lys	Ile	Phe	Gly	Phe		
	930					935					940						
Met	Glu	Glu	Glu	Arg	Lys	Asn	Trp	Gln	Glu	Ala	Arg	Lys	Ala	Cys	Ile		
	945				950					955					960		
Gly	Phe	Gly	Gly	Asn	Leu	Val	Ser	Ile	Gln	Asn	Glu	Lys	Glu	Gln	Ala		
			965						970					975			
Phe	Leu	Thr	Tyr	His	Met	Lys	Asp	Ser	Thr	Phe	Ser	Ala	Trp	Thr	Gly		
		980						985						990			
Leu	Asn	Asp	Val	Asn	Ser	Glu	His	Thr	Phe	Leu	Trp	Thr	Asp	Gly	Arg		
		995					1000						1005				
Gly	Val	His	Tyr	Thr	Asn	Trp	Gly	Lys	Gly	Tyr	Pro	Gly	Gly	Arg			
	1010					1015						1020					
Arg	Ser	Ser	Leu	Ser	Tyr	Glu	Asp	Ala	Asp	Cys	Val	Val	Ile	Ile			
	1025					1030						1035					
Gly	Gly	Ala	Ser	Asn	Glu	Ala	Gly	Lys	Trp	Met	Asp	Asp	Thr	Cys			
	1040					1045						1050					
Asp	Ser	Lys	Arg	Gly	Tyr	Ile	Cys	Gln	Thr	Arg	Ser	Asp	Pro	Ser			
	1055					1060						1065					
Leu	Thr	Asn	Pro	Pro	Ala	Thr	Ile	Gln	Thr	Asp	Gly	Phe	Val	Lys			
	1070					1075						1080					

Tyr	Gly	Lys	Ser	Ser	Tyr	Ser	Leu	Met	Arg	Gln	Lys	Phe	Gln	Trp
	1085					1090					1095			
His	Glu	Ala	Glu	Thr	Tyr	Cys	Lys	Leu	His	Asn	Ser	Leu	Ile	Ala
	1100					1105					1110			
Ser	Ile	Leu	Asp	Pro	Tyr	Ser	Asn	Ala	Phe	Ala	Trp	Leu	Gln	Met
	1115					1120					1125			
Glu	Thr	Ser	Asn	Glu	Arg	Val	Trp	Ile	Ala	Leu	Asn	Ser	Asn	Leu
	1130					1135					1140			
Thr	Asp	Asn	Gln	Tyr	Thr	Trp	Thr	Asp	Lys	Trp	Arg	Val	Arg	Tyr
	1145					1150					1155			
Thr	Asn	Trp	Ala	Ala	Asp	Glu	Pro	Lys	Leu	Lys	Ser	Ala	Cys	Val
	1160					1165					1170			
Tyr	Leu	Asp	Leu	Asp	Gly	Tyr	Trp	Lys	Thr	Ala	His	Cys	Asn	Glu
	1175					1180					1185			
Ser	Phe	Tyr	Phe	Leu	Cys	Lys	Arg	Ser	Asp	Glu	Ile	Pro	Ala	Thr
	1190					1195					1200			
Glu	Pro	Pro	Gln	Leu	Pro	Gly	Arg	Cys	Pro	Glu	Ser	Asp	His	Thr
	1205					1210					1215			
Ala	Trp	Ile	Pro	Phe	His	Gly	His	Cys	Tyr	Tyr	Ile	Glu	Ser	Ser
	1220					1225					1230			
Tyr	Thr	Arg	Asn	Trp	Gly	Gln	Ala	Ser	Leu	Glu	Cys	Leu	Arg	Met
	1235					1240					1245			
Gly	Ser	Ser	Leu	Val	Ser	Ile	Glu	Ser	Ala	Ala	Glu	Ser	Ser	Phe
	1250					1255					1260			
Leu	Ser	Tyr	Arg	Val	Glu	Pro	Leu	Lys	Ser	Lys	Thr	Asn	Phe	Trp
	1265					1270					1275			
Ile	Gly	Leu	Phe	Arg	Asn	Val	Glu	Gly	Thr	Trp	Leu	Trp	Ile	Asn
	1280					1285					1290			
Asn	Ser	Pro	Val	Ser	Phe	Val	Asn	Trp	Asn	Thr	Gly	Asp	Pro	Ser
	1295					1300					1305			
Gly	Glu	Arg	Asn	Asp	Cys	Val	Ala	Leu	His	Ala	Ser	Ser	Gly	Phe
	1310					1315					1320			
Trp	Ser	Asn	Ile	His	Cys	Ser	Ser	Tyr	Lys	Gly	Tyr	Ile	Cys	Lys
	1325					1330					1335			
Arg	Pro	Lys	Ile	Ile	Asp	Ala	Lys	Pro	Thr	His	Glu	Leu	Leu	Thr
	1340					1345					1350			
Thr	Lys	Ala	Asp	Thr	Arg	Lys	Met	Asp	Pro	Ser	Lys			
	1355					1360					1365			

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<210> SEQ ID NO 263
<211> LENGTH: 1370
<212> TYPE: PRT
<213> ORGANISM: Mus musculus
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<400> SEQUENCE: 263

Leu	Leu	Asp	Ala	Arg	Gln	Phe	Leu	Ile	Tyr	Asn	Glu	Asp	His	Lys	Arg
1				5					10					15	
Cys	Val	Asp	Ala	Leu	Ser	Ala	Ile	Ser	Val	Gln	Thr	Ala	Thr	Cys	Asn
			20					25					30		
Pro	Glu	Ala	Glu	Ser	Gln	Lys	Phe	Arg	Trp	Val	Ser	Asp	Ser	Gln	Ile
		35					40					45			
Met	Ser	Val	Ala	Phe	Lys	Leu	Cys	Leu	Gly	Val	Pro	Ser	Lys	Thr	Asp
	50					55					60				
Trp	Ala	Ser	Val	Thr	Leu	Tyr	Ala	Cys	Asp	Ser	Lys	Ser	Glu	Tyr	Gln

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65					70						75					80
Lys	Trp	Glu	Cys	Lys	Asn	Asp	Thr	Leu	Phe	Gly	Ile	Lys	Gly	Thr	Glu	
				85					90					95		
Leu	Tyr	Phe	Asn	Tyr	Gly	Asn	Arg	Gln	Glu	Lys	Asn	Ile	Lys	Leu	Tyr	
			100					105					110			
Lys	Gly	Ser	Gly	Leu	Trp	Ser	Arg	Trp	Lys	Val	Tyr	Gly	Thr	Thr	Asp	
		115					120					125				
Asp	Leu	Cys	Ser	Arg	Gly	Tyr	Glu	Ala	Met	Tyr	Ser	Leu	Leu	Gly	Asn	
	130					135					140					
Ala	Asn	Gly	Ala	Val	Cys	Ala	Phe	Pro	Phe	Lys	Phe	Glu	Asn	Lys	Trp	
145					150					155					160	
Tyr	Ala	Asp	Cys	Thr	Ser	Ala	Gly	Arg	Ser	Asp	Gly	Trp	Leu	Trp	Cys	
				165					170					175		
Gly	Thr	Thr	Thr	Asp	Tyr	Asp	Lys	Asp	Lys	Leu	Phe	Gly	Phe	Cys	Pro	
			180					185					190			
Leu	His	Phe	Glu	Gly	Ser	Glu	Arg	Leu	Trp	Asn	Lys	Asp	Pro	Leu	Thr	
		195					200					205				
Gly	Ile	Leu	Tyr	Gln	Ile	Asn	Ser	Lys	Ser	Ala	Leu	Thr	Trp	His	Gln	
	210					215					220					
Ala	Arg	Ala	Ser	Cys	Lys	Gln	Gln	Asn	Ala	Asp	Leu	Leu	Ser	Val	Thr	
225					230					235					240	
Glu	Ile	His	Glu	Gln	Met	Tyr	Leu	Thr	Gly	Leu	Thr	Ser	Ser	Leu	Ser	
				245					250					255		
Ser	Gly	Leu	Trp	Ile	Gly	Leu	Asn	Ser	Leu	Ser	Val	Arg	Ser	Gly	Trp	
		260						265					270			
Gln	Trp	Ala	Gly	Gly	Ser	Pro	Phe	Arg	Tyr	Leu	Asn	Trp	Leu	Pro	Gly	
		275					280					285				
Ser	Pro	Ser	Ser	Glu	Pro	Gly	Lys	Ser	Cys	Val	Ser	Leu	Asn	Pro	Gly	
	290					295					300					
Lys	Asn	Ala	Lys	Trp	Glu	Asn	Leu	Glu	Cys	Val	Gln	Lys	Leu	Gly	Tyr	
305					310					315				320		
Ile	Cys	Lys	Lys	Gly	Asn	Asn	Thr	Leu	Asn	Pro	Phe	Ile	Ile	Pro	Ser	
				325					330					335		
Ala	Ser	Asp	Val	Pro	Thr	Gly	Cys	Pro	Asn	Gln	Trp	Trp	Pro	Tyr	Ala	
			340					345					350			
Gly	His	Cys	Tyr	Arg	Ile	His	Arg	Glu	Glu	Lys	Lys	Ile	Gln	Lys	Tyr	
		355					360					365				
Ala	Leu	Gln	Ala	Cys	Arg	Lys	Glu	Gly	Gly	Asp	Leu	Ala	Ser	Ile	His	
	370					375					380					
Ser	Ile	Glu	Glu	Phe	Asp	Phe	Ile	Phe	Ser	Gln	Leu	Gly	Tyr	Glu	Pro	
385					390					395				400		
Asn	Asp	Glu	Leu	Trp	Ile	Gly	Leu	Asn	Asp	Ile	Lys	Ile	Gln	Met	Tyr	
				405					410					415		
Phe	Glu	Trp	Ser	Asp	Gly	Thr	Pro	Val	Thr	Phe	Thr	Lys	Trp	Leu	Pro	
			420					425					430			
Gly	Glu	Pro	Ser	His	Glu	Asn	Asn	Arg	Gln	Glu	Asp	Cys	Val	Val	Met	
		435					440					445				
Lys	Gly	Lys	Asp	Gly	Tyr	Trp	Ala	Asp	Arg	Ala	Cys	Glu	Gln	Pro	Leu	
	450					455					460					
Gly	Tyr	Ile	Cys	Lys	Met	Val	Ser	Gln	Ser	His	Ala	Val	Val	Pro	Glu	
465					470					475				480		
Gly	Ala	Asp	Lys	Gly	Cys	Arg	Lys	Gly	Trp	Lys	Arg	His	Gly	Phe	Tyr	
				485					490					495		

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Cys	Tyr	Leu	Ile	Gly	Ser	Thr	Leu	Ser	Thr	Phe	Thr	Asp	Ala	Asn	His
		500						505					510		
Thr	Cys	Thr	Asn	Glu	Lys	Ala	Tyr	Leu	Thr	Thr	Val	Glu	Asp	Arg	Tyr
		515						520				525			
Glu	Gln	Ala	Phe	Leu	Thr	Ser	Leu	Val	Gly	Leu	Arg	Pro	Glu	Lys	Tyr
		530				535					540				
Phe	Trp	Thr	Gly	Leu	Ser	Asp	Val	Gln	Asn	Lys	Gly	Thr	Phe	Arg	Trp
545					550					555					560
Thr	Val	Asp	Glu	Gln	Val	Gln	Phe	Thr	His	Trp	Asn	Ala	Asp	Met	Pro
				565					570					575	
Gly	Arg	Lys	Ala	Gly	Cys	Val	Ala	Met	Lys	Thr	Gly	Val	Ala	Gly	Gly
			580					585					590		
Leu	Trp	Asp	Val	Leu	Ser	Cys	Glu	Glu	Lys	Ala	Lys	Phe	Val	Cys	Lys
		595					600					605			
His	Trp	Ala	Glu	Gly	Val	Thr	Arg	Pro	Pro	Glu	Pro	Thr	Thr	Thr	Pro
	610					615					620				
Glu	Pro	Lys	Cys	Pro	Glu	Asn	Trp	Gly	Thr	Thr	Ser	Lys	Thr	Ser	Met
625					630					635					640
Cys	Phe	Lys	Leu	Tyr	Ala	Lys	Gly	Lys	His	Glu	Lys	Lys	Thr	Trp	Phe
			645						650					655	
Glu	Ser	Arg	Asp	Phe	Cys	Lys	Ala	Ile	Gly	Gly	Glu	Leu	Ala	Ser	Ile
			660					665					670		
Lys	Ser	Lys	Asp	Glu	Gln	Gln	Val	Ile	Trp	Arg	Leu	Ile	Thr	Ser	Ser
		675					680					685			
Gly	Ser	Tyr	His	Glu	Leu	Phe	Trp	Leu	Gly	Leu	Thr	Tyr	Gly	Ser	Pro
	690					695					700				
Ser	Glu	Gly	Phe	Thr	Trp	Ser	Asp	Gly	Ser	Pro	Val	Ser	Tyr	Glu	Asn
705					710					715					720
Trp	Ala	Tyr	Gly	Glu	Pro	Asn	Asn	Tyr	Gln	Asn	Val	Glu	Tyr	Cys	Gly
			725						730					735	
Glu	Leu	Lys	Gly	Asp	Pro	Gly	Met	Ser	Trp	Asn	Asp	Ile	Asn	Cys	Glu
			740					745					750		
His	Leu	Asn	Asn	Trp	Ile	Cys	Gln	Ile	Gln	Lys	Gly	Lys	Thr	Leu	Leu
		755					760					765			
Pro	Glu	Pro	Thr	Pro	Ala	Pro	Gln	Asp	Asn	Pro	Pro	Val	Thr	Ala	Asp
	770					775					780				
Gly	Trp	Val	Ile	Tyr	Lys	Asp	Tyr	Gln	Tyr	Tyr	Phe	Ser	Lys	Glu	Lys
785					790					795					800
Glu	Thr	Met	Asp	Asn	Ala	Arg	Ala	Phe	Cys	Lys	Lys	Asn	Phe	Gly	Asp
			805					810						815	
Leu	Ala	Thr	Ile	Lys	Ser	Glu	Ser	Glu	Lys	Lys	Phe	Leu	Trp	Lys	Tyr
			820					825					830		
Ile	Asn	Lys	Asn	Gly	Gly	Gln	Ser	Pro	Tyr	Phe	Ile	Gly	Met	Leu	Ile
		835					840					845			
Ser	Met	Asp	Lys	Lys	Phe	Ile	Trp	Met	Asp	Gly	Ser	Lys	Val	Asp	Phe
	850					855					860				
Val	Ala	Trp	Ala	Thr	Gly	Glu	Pro	Asn	Phe	Ala	Asn	Asp	Asp	Glu	Asn
865					870					875					880
Cys	Val	Thr	Met	Tyr	Thr	Asn	Ser	Gly	Phe	Trp	Asn	Asp	Ile	Asn	Cys
			885						890					895	
Gly	Tyr	Pro	Asn	Asn	Phe	Ile	Cys	Gln	Arg	His	Asn	Ser	Ser	Ile	Asn
			900					905						910	

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Ala Thr Ala Met Pro Thr Thr Pro Thr Thr Pro Gly Gly Cys Lys Glu	
915	920 925
Gly Trp His Leu Tyr Lys Asn Lys Cys Phe Lys Ile Phe Gly Phe Ala	
930	935 940
Asn Glu Glu Lys Lys Ser Trp Gln Asp Ala Arg Gln Ala Cys Lys Gly	
945	950 955 960
Leu Lys Gly Asn Leu Val Ser Ile Glu Asn Ala Gln Glu Gln Ala Phe	
	965 970 975
Val Thr Tyr His Met Arg Asp Ser Thr Phe Asn Ala Trp Thr Gly Leu	
	980 985 990
Asn Asp Ile Asn Ala Glu His Met Phe Leu Trp Thr Ala Gly Gln Gly	
	995 1000 1005
Val His Tyr Thr Asn Trp Gly Lys Gly Tyr Pro Gly Gly Arg Arg	
1010	1015 1020
Ser Ser Leu Ser Tyr Glu Asp Ala Asp Cys Val Val Ile Gly	
1025	1030 1035
Gly Asn Ser Arg Glu Ala Gly Thr Trp Met Asp Asp Thr Cys Asp	
1040	1045 1050
Ser Lys Gln Gly Tyr Ile Cys Gln Thr Gln Thr Asp Pro Ser Leu	
1055	1060 1065
Pro Val Ser Pro Thr Thr Thr Pro Lys Asp Gly Phe Val Thr Tyr	
1070	1075 1080
Gly Lys Ser Ser Tyr Ser Leu Met Lys Leu Lys Leu Pro Trp His	
1085	1090 1095
Glu Ala Glu Thr Tyr Cys Lys Asp His Thr Ser Leu Leu Ala Ser	
1100	1105 1110
Ile Leu Asp Pro Tyr Ser Asn Ala Phe Ala Trp Met Lys Met His	
1115	1120 1125
Pro Phe Asn Val Pro Ile Trp Ile Ala Leu Asn Ser Asn Leu Thr	
1130	1135 1140
Asn Asn Glu Tyr Thr Trp Thr Asp Arg Trp Arg Val Arg Tyr Thr	
1145	1150 1155
Asn Trp Gly Ala Asp Glu Pro Lys Leu Lys Ser Ala Cys Val Tyr	
1160	1165 1170
Met Asp Val Asp Gly Tyr Trp Arg Thr Ser Tyr Cys Asn Glu Ser	
1175	1180 1185
Phe Tyr Phe Leu Cys Lys Lys Ser Asp Glu Ile Pro Ala Thr Glu	
1190	1195 1200
Pro Pro Gln Leu Pro Gly Lys Cys Pro Glu Ser Glu Gln Thr Ala	
1205	1210 1215
Trp Ile Pro Phe Tyr Gly His Cys Tyr Tyr Phe Glu Ser Ser Phe	
1220	1225 1230
Thr Arg Ser Trp Gly Gln Ala Ser Leu Glu Cys Leu Arg Met Gly	
1235	1240 1245
Ala Ser Leu Val Ser Ile Glu Thr Ala Ala Glu Ser Ser Phe Leu	
1250	1255 1260
Ser Tyr Arg Val Glu Pro Leu Lys Ser Lys Thr Asn Phe Trp Ile	
1265	1270 1275
Gly Met Phe Arg Asn Val Glu Gly Lys Trp Leu Trp Leu Asn Asp	
1280	1285 1290
Asn Pro Val Ser Phe Val Asn Trp Lys Thr Gly Asp Pro Ser Gly	
1295	1300 1305
Glu Arg Asn Asp Cys Val Val Leu Ala Ser Ser Ser Gly Leu Trp	

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1310	1315	1320
Asn Asn Ile His Cys Ser Ser Tyr Lys Gly Phe Ile Cys Lys Met		
1325	1330	1335
Pro Lys Ile Ile Asp Pro Val Thr Thr His Ser Ser Ile Thr Thr		
1340	1345	1350
Lys Ala Asp Gln Arg Lys Met Asp Pro Gln Pro Lys Gly Ser Ser		
1355	1360	1365
Lys Ala		
1370		

What is claimed is:

1. A method of in vivo imaging tumor-associated macrophages (TAM) in a subject, the method comprising:

administering to the subject an immunoglobulin single variable domain labeled with a detectable label, wherein the immunoglobulin single variable domain specifically binds to a macrophage mannose receptor selected from the group consisting of SEQ ID NO: 260 and SEQ ID NO: 258, and wherein the immunoglobulin single variable domain comprises a nanobody sequence (V_{HH}) selected from the group consisting of SEQ ID NO: 4, SEQ ID NO: 130, SEQ ID NO: 131, SEQ ID NO: 137, SEQ ID NO: 139, SEQ ID NO: 141, and SEQ ID NO: 144, and

Imaging TAM in the subject to which the labeled immunoglobulin single variable domain binds.

2. The method according to claim 1, the method further comprising:

co-administering to the subject an unlabeled bivalent form of the immunoglobulin single variable domain to block extratumoral binding sites for the immunoglobulin single variable domain in the subject.

3. The method according to claim 2, wherein the imaged TAM are MHC Π^{low} .

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4. The method according to claim 1, wherein the subject is mammalian.

5. The method according to claim 4, wherein the subject is human.

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6. The method according to claim 1, wherein the imaged TAM are located in the hypoxic regions of a solid tumor.

7. The method according to claim 1, wherein the imaged TAM are associated with mammary adenocarcinoma cells or lung carcinoma cells.

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8. The method according to claim 1, wherein the nanobody sequence comprises SEQ ID NO:4.

9. The method according to claim 1, wherein the nanobody sequence comprises SEQ ID NO:130.

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10. The method according to claim 1, wherein the nanobody sequence comprises SEQ ID NO:131.

11. The method according to claim 1, wherein the nanobody sequence comprises SEQ ID NO:137.

12. The method according to claim 1, wherein the nanobody sequence comprises SEQ ID NO:139.

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13. The method according to claim 1, wherein the nanobody sequence comprises SEQ ID NO:141.

14. The method according to claim 1, wherein the nanobody sequence comprises SEQ ID NO:144.

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